



## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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<b>(30) Priority Data:</b> 08/835,913 10 April 1997 (10.04.97) US			
<b>(71) Applicant:</b> GENETICS INSTITUTE, INC. [US/US]; 87 CambridgePark Drive, Cambridge, MA 02140 (US).			
<b>(72) Inventors:</b> JACOBS, Kenneth; 151 Beaumont Avenue, Newton, MA 02160 (US). MCCOY, John, M.; 56 Howard Street, Reading, MA 01867 (US). LAVALLIE, Edward, R.; 113 Ann Lee Road, Harvard, MA 01451 (US). RACIE, Lisa, A.; 124 School Street, Acton, MA 01720 (US). MERBERG, David; 2 Orchard Drive, Acton, MA 01720 (US). TREACY, Maurice; 93 Walcott Road, Chestnut Hill, MA 02167 (US). SPAULDING, Vikki; 11 Meadowbank Road, Billerica, MA 01821 (US). AGOSTINO, Michael, J.; 26 Wolcott Avenue, Andover, MA 01810 (US).			
<b>(74) Agent:</b> SPRUNGER, Suzanne, A.; Genetics Institute, Inc., 87 CambridgePark Drive, Cambridge, MA 02140 (US).			<b>Published</b> <i>Without international search report and to be republished upon receipt of that report.</i>
<b>(54) Title:</b> SECRETED EXPRESSED SEQUENCE TAGS (sESTs)			
<b>(57) Abstract</b>  Secreted expressed sequence tags (sESTs) isolated from a variety of human tissue sources are provided.			

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<b>(54) Title:</b> SECRETED EXPRESSED SEQUENCE TAGS (sESTs)  <b>(57) Abstract</b>  Secreted expressed sequence tags (sESTs) isolated from a variety of human tissue sources are provided.		

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## SECRETED EXPRESSED SEQUENCE TAGS (sESTs)

FIELD OF THE INVENTION

5           The present invention provides novel polynucleotides which are expressed sequence tags (ESTs) for secreted proteins.

BACKGROUND OF THE INVENTION

10           Gargantuan efforts have been employed by various investigational projects to randomly sequence portions of naturally-occurring cDNAs. The rationale behind this approach to identification and sequencing genes is founded in two basic principles: (1) that transcribed cDNAs represent the product of the most important genes, namely those that are actually expressed *in vivo*, and (2) that efforts to sequence genes and other portions of the genome of target organisms which are not actually expressed wastes substantial effort on areas not likely  
15           to yield genetic information of therapeutic importance. Thus, the high-throughput sequencing efforts focus on only those portions of the genome which are expressed. The randomly produced cDNA sequences represent "expressed sequence tags" or "ESTs", which identify and can be used as probes for the longer, full-length cDNA or genomic sequence from which they were transcribed.

20           Although this "shortcut" approach to genomic sequencing presents savings of effort compared to sequencing of the complete genome, it still produced a vast array of ESTs which may not be directly useful as protein therapeutics. To date, the majority of protein-related drug discovery has focused on the use of secreted proteins to produce a desired therapeutic effect. Since the EST approach theoretically identifies all expressed proteins, it produces an EST  
25           library which contains a mixture of secreted proteins (such as hormones, cytokines and receptors) and non-secreted proteins (such as, for example, metabolic enzymes and cellular structural proteins), without identifying which ESTs correspond to proteins falling into either category. As a result, these methods are not optimally tailored to the needs of investigators searching for secreted proteins because they must separate the secreted "wheat" from the non-  
30           secreted "chaff", wasting effort and resources in the process.

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Co-assigned U.S. Patent No. 5,536,637, which is incorporated herein by reference, provides methods for focusing genomic sequencing efforts on sequences encoding the secreted proteins which are of most interest for identification of protein therapeutics. The '637 patent discloses a "signal sequence trap" which selectively identifies ESTs for secreted proteins,  
5 namely "secreted expressed sequence tags" or "sESTs". It is to these sESTs that the present invention is directed.

### SUMMARY OF THE INVENTION

The present invention provides for sESTs isolated from a variety of human RNA/cDNA sources.

In preferred embodiments, the present invention provides an isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

5                   SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID

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or a complement of said sequence.

In other embodiments, the present invention provides an isolated polynucleotide  
 consisting of a nucleotide sequence selected from the group consisting of:

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or a complement of said sequence.

20 In further embodiments, the present invention provides an isolated polynucleotide  
 consisting essentially of a nucleotide sequence selected from the group consisting of:

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or a complement of said sequence.

In yet other embodiments, the present invention provides an isolated polynucleotide  
 comprising a nucleotide sequence which hybridizes to a sequence selected from the group  
 30 consisting of:

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or to a complement of said sequence.

The invention also provides for proteins encoded by the above-described  
5 polynucleotides.

### DETAILED DESCRIPTION

The nucleotide sequences of the sESTs of the present invention are reported in the Sequence Listing below. Table 2 lists the "Clone ID Nos." assigned by applicants to each  
10 SEQ ID NO: in the Sequence Listing.

Table 2

Each pair of entries in this table consists of the SEQ ID NO (e.g., 1, 2, etc.) followed by the Clone ID No. for such sequence (e.g., B11, B18, etc.).

15	1	B11	21	C3	41	C639	61	D148
	2	B18	22	C32	42	C641	62	D154
	3	B21	23	C141	43	C642	63	D167
	4	B26	24	C143	44	C645	64	D179
	5	B40	25	C180	45	D4	65	D188
20	6	B115	26	C195	46	D7	66	D196
	7	B121	27	C293	47	D14	67	D200
	8	B124	28	C312	48	D15	68	D203
	9	B125	29	C539	49	D27	69	D233
	10	B142	30	C544	50	D68	70	D252
25	11	B196	31	C547	51	D69	71	D286
	12	B208	32	C571	52	D81	72	D303
	13	B224	33	C604	53	D100	73	D304
	14	B227	34	C607	54	D101	74	D305
	15	B232	35	C608	55	D104	75	D310
30	16	B236	36	C610	56	D105	76	D311
	17	B238	37	C617	57	D115	77	D318
	18	B255	38	C626	58	D121	78	D327
	19	C1	39	C627	59	D133	79	D329
20	20	C2	40	C636	60	D143	80	E1

	81	E4	115	H291	149	J139	183	M141
	82	E5	116	H306	150	J143	184	M152
	83	E11	117	H383	151	J156	185	M194
	84	E12	118	H426	152	J168	186	M230
5	85	E14	119	H438	153	J297	187	M273
	86	E18	120	H541	154	J317	188	M292
	87	G1	121	H545	155	J322	189	M301
	88	G12	122	H657	156	J422	190	M313
	89	G16	123	H698	157	J435	191	M328
10	90	G20	124	H758	158	J509	192	M338
	91	G21	125	H770	159	J512	193	O7
	92	G26	126	H849	160	J532	194	O47
	93	G31	127	H920	161	J546	195	O67
	94	G40	128	H978	162	J598	196	O75
15	95	G46	129	H999	163	J635	197	O99
	96	G53	130	H1004	164	J638	198	O135
	97	G55	131	H1010	165	J708	199	O139
	98	G58	132	H1045	166	J731	200	O268
	99	G68	133	H1052	167	M4	201	O276
20	100	G85	134	H1075	168	M6	202	O289
	101	G86	135	H1096	169	M43	203	O338
	102	G99	136	H1116	170	M60	204	O349
	103	G103	137	H1165	171	M68	205	O351
	104	G107	138	H1301	172	M71	206	O372
25	105	G108	139	H1408	173	M88	207	O386
	106	G112	140	H1413	174	M97	208	O417
	107	G114	141	H1456	175	M100	209	O418
	108	H45	142	I5	176	M114	210	O463
	109	H162	143	I28	177	M120	211	S10
30	110	H165	144	I32	178	M121	212	S34
	111	H171	145	J5	179	M125	213	S70
	112	H174	146	J54	180	M126	214	S169
	113	H225	147	J66	181	M128	215	S185
	114	H236	148	J135	182	M137	216	S195

	217	AA20	251	AJ6	285	AM72	319	AP137
	218	AA35	252	AJ8	286	AM93	320	AP76
	219	AB10	253	AJ52	287	AK679	321	AP87
	220	AA240	254	AJ53	288	AK684	322	AP90
5	221	AA244	255	AJ54	289	AK699	323	AP150
	222	AA246	256	AJ78	290	AM155	324	AP159
	223	AA287	257	AJ80	291	AM167	325	AP160
	224	AA299	258	AK368	292	AM207	326	AP162
	225	AA318	259	AJ127	293	AM217	327	AP168
10	226	AB45	260	AJ142	294	AM224	328	AP179
	227	AA36	261	AJ143	295	AM226	329	AP197
	228	AA363	262	AC339	296	AM235	330	AP215
	229	AA365	263	AC370	297	AM259	331	AP224
	230	AA351	264	AL14	298	AM266	332	AP226
15	231	AB290	265	AK401	299	AM267	333	AP242
	232	AC41	266	AK438	300	AM277	334	AP250
	233	AC18	267	AK583	301	AM279	335	AQ11
	234	AC175	268	AK585	302	AC387	336	AQ2
	235	AC114	269	AK598	303	AC395	337	AQ21
20	236	AC111	270	AK604	304	AC410	338	AQ23
	237	AC100	271	AK609	305	AC412	339	AQ3
	238	AC222	272	AK620	306	AC423	340	AQ34
	239	AC325	273	AM10	307	AJ146	341	AQ5
	240	AI44	274	AM104	308	AJ147	342	AR15
25	241	AI6	275	AM123	309	AJ156	343	AR22
	242	AI86	276	AM137	310	AJ168	344	AR28
	243	AJ1	277	AM15	311	AJ169	345	AR3
	244	AJ10	278	AM16	312	AJ172	346	AR34
	245	AJ13	279	AM30	313	AJ173	347	AR42
30	246	AJ15	280	AM38	314	AJ174	348	AR54
	247	AJ20	281	AM39	315	AK528	349	AR61
	248	AJ21	282	AM42	316	AP116	350	AM282
	249	AJ26	283	AM46	317	AP120	351	AM307
	250	AJ27	284	AM66	318	AP135	352	AM349

	353	AM372	387	AR310	421	AM616	455	AM921
	354	AM392	388	AR323	422	AM622	456	AM931
	355	AM400	389	AR324	423	AM625	457	AM973
	356	AM430	390	AR325	424	AM666	458	AM996
5	357	AP11	391	AR349	425	AM686	459	AS56
	358	AP2	392	AR360	426	AM704	460	AS61
	359	AP56	393	AR364	427	AM726	461	AS63
	360	AP57	394	AR400	428	AM728	462	AS65
	361	AP58	395	AR415	429	AM735	463	AS83
10	362	AP60	396	AR417	430	AM741	464	AS85
	363	AP67	397	AM558	431	AM742	465	AS86
	364	AP7	398	AM566	432	AM754	466	AS88
	365	AQ53	399	AM600	433	AM781	467	AT107
	366	AQ54	400	AR420	434	AM795	468	AT111
15	367	AQ61	401	AR437	435	AM814	469	AT138
	368	AQ64	402	AR440	436	AM833	470	AT140
	369	AQ71	403	AR446	437	AM838	471	AT142
	370	AQ73	404	AR450	438	AT16	472	AT146
	371	AQ83	405	AR452	439	AT19	473	AT151
20	372	AM1075	406	AR455	440	AT20	474	AT157
	373	AM1076	407	AR463	441	AT4	475	AT181
	374	AM1083	408	AR464	442	AT53	476	AT97
	375	AR100	409	AR467	443	AT63	477	AS239
	376	AR69	410	AR474	444	AT64	478	AT226
25	377	AM1017	411	AR475	445	AT74	479	AT259
	378	AM1032	412	AS15	446	AT94	480	AT260
	379	AM1036	413	AS20	447	AT95	481	AT265
	380	AM1045	414	AS23	448	AM1000	482	AT280
	381	AM1060	415	AS31	449	AM856	483	AT340
30	382	AM1067	416	AS47	450	AM885	484	AT351
	383	AR253	417	AS48	451	AM889	485	AT352
	384	AK642	418	AS7	452	AM892	486	AT356
	385	AK647	419	AM610	453	AM910	487	AT359
	386	AK650	420	AM614	454	AM918	488	AT361

	489	AS252	523	AU161	557	AW106	591	BE28
	490	AS263	524	AU164	558	AW107	592	BE3
	491	AS264	525	AZ285	559	AW109	593	BE34
	492	AS268	526	AZ286	560	AW133	594	BE9
5	493	AS271	527	AZ287	561	AW140	595	AZ12
	494	AS294	528	AZ290	562	AW92	596	AZ22
	495	AS301	529	AZ188	563	AW95	597	AZ32
	496	AS330	530	AZ191	564	AW98	598	AZ45
	497	AS144	531	AZ204	565	BA185	599	AZ46
10	498	AS152	532	AZ219	566	BA204	600	BF143
	499	AS157	533	AW170	567	BA210	601	BF146
	500	AS162	534	AW176	568	BA226	602	BF157
	501	AS164	535	AW178	569	BG1	603	BF160
	502	AS167	536	AW179	570	BG13	604	BF169
15	503	AS180	537	AW182	571	BG3	605	BF171
	504	AS186	538	AW185	572	BG33	606	BF176
	505	AS187	539	AW189	573	BG36	607	BF178
	506	AU36	540	AW192	574	BG37	608	AS196
	507	AU39	541	AW194	575	BG40	609	AS202
20	508	AU43	542	AW199	576	BG43	610	AS209
	509	AU47	543	AW222	577	BG48	611	AS216
	510	AU50	544	AW231	578	BG58	612	AS230
	511	AU59	545	AZ261	579	BG72	613	AS232
	512	AU71	546	AZ264	580	BG73	614	AX101
25	513	AU101	547	AZ302	581	BF101	615	AX104
	514	AU102	548	AZ303	582	BF132	616	AX107
	515	AU105	549	AK649	583	AZ69	617	AX109
	516	AU106	550	AK663	584	BD51	618	AX122
	517	AU107	551	AR336	585	BD53	619	AX124
30	518	AU115	552	AR356	586	BD65	620	AX127
	519	AU118	553	AR398	587	BD66	621	AX128
	520	AU122	554	AR399	588	BD73	622	AX130
	521	AU138	555	AM1016	589	BD77	623	AX132
	522	AU139	556	AW105	590	BD80	624	AX136

	625	AX137	659	BG274	693	AW33	727	BG504
	626	AX143	660	BG276	694	AW36	728	BG510
	627	AX146	661	AX12	695	AW47	729	BG511
	628	AX51	662	AX17	696	AW49	730	BG513
5	629	AX55	663	AX256	697	AW52	731	BG516
	630	AX56	664	AX30	698	AW60	732	BG518
	631	AX60	665	AX32	699	AW66	733	BG526
	632	AX65	666	AX34	700	AW76	734	BG528
	633	AX78	667	AX49	701	AY241	735	BG552
10	634	AX80	668	AX6	702	AY259	736	BG553
	635	AX81	669	AX8	703	AY268	737	BG556
	636	AX92	670	AZ180	704	BA123	738	AX309
	637	AX97	671	BG191	705	BA134	739	AX315
	638	AX98	672	BG193	706	BA170	740	AX318
15	639	AX99	673	BG199	707	BA176	741	AY186
	640	AZ109	674	BG201	708	BA178	742	AY190
	641	AZ114	675	BG219	709	BA179	743	AY200
	642	BF286	676	BG220	710	BA216	744	AY208
	643	BF290	677	BG221	711	BA233	745	AY211
20	644	BF314	678	BG225	712	BD372	746	AY283
	645	BG236	679	BG228	713	BD375	747	AY289
	646	BG237	680	BG442	714	BD379	748	AY304
	647	BG240	681	BG449	715	BD380	749	AY307
	648	BG241	682	BG457	716	BD403	750	AY318
25	649	BG248	683	BG458	717	BD407	751	AY333
	650	BG249	684	BG461	718	BD409	752	AY334
	651	BG250	685	BG465	719	BD413	753	AY342
	652	BG251	686	BG467	720	BD414	754	AY358
	653	BG255	687	BG471	721	BG481	755	AY362
30	654	BG260	688	BG59	722	BG482	756	BF190
	655	BG267	689	AW12	723	BG492	757	BF191
	656	BG271	690	AW22	724	BG494	758	BF193
	657	BG272	691	AW24	725	BG495	759	BF197
	658	BG273	692	AW32	726	BG503	760	BF208



	761	BF211	795	BG373	829	BD174	863	BI17
	762	BF216	796	BG374	830	BD176	864	BI2
	763	BF221	797	BG379	831	BD177	865	BI24
	764	BF227	798	BG386	832	BD178	866	BI25
5	765	BF228	799	BG388	833	BD183	867	BI3
	766	BF245	800	BG389	834	BE50	868	BI36
	767	BF250	801	BG391	835	BE64	869	BI37
	768	BF258	802	BG393	836	BE89	870	BI39
	769	BF259	803	BG396	837	BG490	871	BI40
10	770	BF263	804	BG409	838	BG491	872	BI41
	771	BF270	805	BG411	839	BG501	873	BI46
	772	BF273	806	BG414	840	BG502	874	BM1
	773	BG280	807	BG420	841	BG512	875	BM17
	774	BG283	808	HW105	842	BG532	876	BM4
15	775	BG284	809	BB54	843	BK162	877	BM41
	776	BG288	810	BD101	844	BK165	878	BM46
	777	BG296	811	BD104	845	BK167	879	BM69
	778	BG305	812	BD107	846	BK171	880	BM88
	779	BG306	813	BD109	847	BK179	881	BM90
20	780	BG309	814	BD119	848	BK180	882	BA106
	781	BG324	815	BD121	849	BK183	883	BA12
	782	BG327	816	BD127	850	BK186	884	BA32
	783	BG329	817	BD128	851	BK194	885	BA38
	784	BG332	818	BD132	852	BK200	886	BA40
25	785	BG334	819	BD136	853	BK206	887	BA71
	786	BG335	820	BD137	854	BK216	888	BA79
	787	BG350	821	BD140	855	BK231	889	BA8
	788	BG356	822	BD144	856	BK232	890	BA88
	789	BG357	823	BD151	857	BK236	891	BA90
30	790	BG363	824	BD154	858	BK237	892	BA91
	791	BG365	825	BD164	859	BK241	893	BA98
	792	BG366	826	BD165	860	BK243	894	BK15
	793	BG368	827	BD169	861	BK246	895	BK17
	794	BG372	828	BD170	862	BK253	896	BK24

	897	BK257	931	AY428	965	BK146	999	BG139
	898	BK26	932	AY437	966	BK155	1000	BG140
	899	BK260	933	AY440	967	BK158	1001	BG141
	900	BK265	934	AY442	968	BK75	1002	BG142
5	901	BK270	935	AY449	969	BK78	1003	BG145
	902	BK271	936	AY457	970	BK92	1004	BG148
	903	BK280	937	AY470	971	BK93	1005	BG151
	904	BK284	938	AY487	972	BK95	1006	BG156
	905	BK286	939	AY489	973	BK96	1007	BG158
10	906	BK29	940	AY511	974	BM101	1008	BG160
	907	BK291	941	BE153	975	BM117	1009	BG168
	908	BK295	942	BF327	976	BM124	1010	BG170
	909	BK296	943	BI64	977	BM139	1011	BG171
	910	BK299	944	BI66	978	BM154	1012	BG172
15	911	BK304	945	BI75	979	BM155	1013	BG173
	912	BK307	946	BI80	980	BM158	1014	BG93
	913	BK308	947	BI81	981	BM94	1015	BG95
	914	BK339	948	BI82	982	AY102	1016	BI102
	915	BK34	949	BI86	983	AY107	1017	BI103
20	916	BK343	950	BI87	984	AY122	1018	BI107
	917	BK40	951	BI88	985	AY131	1019	BI110
	918	BK41	952	BI91	986	AY137	1020	BI114
	919	BK48	953	BI92	987	AY140	1021	BI117
	920	BK49	954	BK102	988	AY147	1022	BI120
25	921	BK57	955	BK105	989	AY157	1023	BI122
	922	BK59	956	BK107	990	AY160	1024	BI124
	923	BK61	957	BK112	991	AY183	1025	BI126
	924	BK68	958	BK114	992	AY93	1026	BI127
	925	BL341	959	BK115	993	BG102	1027	BI129
30	926	AY398	960	BK117	994	BG104	1028	BI133
	927	AY406	961	BK120	995	BG112	1029	BI139
	928	AY407	962	BK130	996	BG125	1030	BI150
	929	AY408	963	BK134	997	BG132	1031	BI164
	930	AY421	964	BK142	998	BG137	1032	BI97

	1033	BI98	1067	BQ58	1101	BO71	1135	BL209
	1034	BI99	1068	BD189	1102	BO87	1136	BL210
	1035	BS1	1069	BD194	1103	BO9	1137	BL211
	1036	BS54	1070	BD199	1104	BD235	1138	BL219
5	1037	BS58	1071	BD200	1105	BD240	1139	BL220
	1038	BS81	1072	BD201	1106	BD241	1140	BL229
	1039	BS89	1073	BD208	1107	BD244	1141	BL230
	1040	BH100	1074	BD209	1108	BD247	1142	BL243
	1041	BH106	1075	BD213	1109	BD251	1143	BL247
10	1042	BH111	1076	BD214	1110	BD257	1144	BL249
	1043	BH123	1077	BD222	1111	BD260	1145	BL255
	1044	BH131	1078	BH19	1112	BD262	1146	BL257
	1045	BH157	1079	BH195	1113	BD265	1147	BL271
	1046	BH297	1080	BH2	1114	BD268	1148	BL274
15	1047	BH306	1081	BH227	1115	BD522	1149	BL30
	1048	BH309	1082	BH272	1116	BD538	1150	BL67
	1049	BH316	1083	BH276	1117	BD544	1151	BL73
	1050	BH323	1084	BH281	1118	BD548	1152	BL89
	1051	BH339	1085	BH41	1119	BD561	1153	BD420
20	1052	BH365	1086	BH51	1120	BL147	1154	BD423
	1053	BH389	1087	BH66	1121	BL15	1155	BD426
	1054	BH392	1088	BH7	1122	BL152	1156	BD427
	1055	BJ54	1089	BH87	1123	BL156	1157	BD428
	1056	BJ62	1090	BH90	1124	BL160	1158	BD438
25	1057	BJ66	1091	BJ20	1125	BL178	1159	BD441
	1058	BJ67	1092	BJ27	1126	BL179	1160	BD445
	1059	BJ69	1093	BJ29	1127	BL183	1161	BD473
	1060	BJ70	1094	BJ38	1128	BL185	1162	BD486
	1061	BJ75	1095	BJ39	1129	BL186	1163	BD489
30	1062	BJ76	1096	BJ9	1130	BL187	1164	BD492
	1063	BJ78	1097	BO11	1131	BL194	1165	BD512
	1064	BJ87	1098	BO20	1132	BL196	1166	BL106
	1065	BQ20	1099	BO4	1133	BL201	1167	BL310
	1066	BQ3	1100	BO52	1134	BL205	1168	BN1

	1169	BN107	1203	BD351	1237	BN351	1271	BP22
	1170	BN12	1204	BN189	1238	BN354	1272	BP24
	1171	BN130	1205	BN201	1239	BN365	1273	BP25
	1172	BN132	1206	BN212	1240	BN422	1274	BT99
5	1173	BN133	1207	BN280	1241	BN425	1275	BP28
	1174	BN139	1208	BN284	1242	BN439	1276	BP3
	1175	BN141	1209	BN329	1243	BN460	1277	BP4
	1176	BN153	1210	BN331	1244	BN461	1278	BP43
	1177	BN156	1211	BN591	1245	BN463	1279	BP47
10	1178	BN171	1212	BO153	1246	BN472	1280	BP504
	1179	BN174	1213	BO157	1247	BN473	1281	BP506
	1180	BN180	1214	BO159	1248	BO100	1282	BP508
	1181	BN246	1215	BO166	1249	BO107	1283	BP521
	1182	BN267	1216	BO178	1250	BO114	1284	BP528
15	1183	BN268	1217	BO189	1251	BO121	1285	BP530
	1184	BN33	1218	BO194	1252	BO126	1286	BP532
	1185	BN40	1219	BO210	1253	BO133	1287	BP537
	1186	BN48	1220	BO212	1254	BO137	1288	BP544
	1187	BN5	1221	BO213	1255	BO398	1289	BP545
20	1188	BN563	1222	BO218	1256	BO399	1290	BP55
	1189	BN65	1223	BO226	1257	BO401	1291	BP567
	1190	BN69	1224	BO279	1258	BO432	1292	BP569
	1191	BN81	1225	BO301	1259	BO528	1293	BP57
	1192	BN97	1226	BO323	1260	BO535	1294	BP590
25	1193	BN99	1227	BO358	1261	BO538	1295	BP61
	1194	BD286	1228	BO365	1262	BO549	1296	BP70
	1195	BD288	1229	BO385	1263	BO551	1297	BP71
	1196	BD297	1230	BO250	1264	BO93	1298	BP780
	1197	BD316	1231	BO254	1265	BP101	1299	BP783
30	1198	BD317	1232	BO256	1266	BP118	1300	BP784
	1199	BD321	1233	BO260	1267	BP121	1301	BP791
	1200	BD327	1234	BO261	1268	BP15	1302	BP797
	1201	BD335	1235	BO273	1269	BP19	1303	BP806
	1202	BD339	1236	BN342	1270	BP21	1304	BP809

	1305	BP810	1339	BV243	1373	CC71	1407	BR572
	1306	BP813	1340	BV248	1374	CC76	1408	BR559
	1307	BP814	1341	BV250	1375	CC78	1409	BR538
	1308	BP815	1342	BV259	1376	CC81	1410	BR537
5	1309	BP820	1343	BV273	1377	CC89	1411	BR533
	1310	BP84	1344	BV275	1378	CD124	1412	BR500
	1311	BP919	1345	BV49	1379	CD128	1413	BR48
	1312	BP925	1346	BV51	1380	CD140	1414	BR475
	1313	BQ115	1347	BV66	1381	CD145	1415	BR436
10	1314	BQ129	1348	BV70	1382	CD146	1416	BR434
	1315	BS116	1349	BV71	1383	CD173	1417	BR4
	1316	BT101	1350	BV72	1384	CD194	1418	BR346
	1317	BT133	1351	BV73	1385	CD31	1419	BR342
	1318	BT139	1352	BV88	1386	CD50	1420	BR338
15	1319	BT33	1353	BW345	1387	CF50	1421	BR333
	1320	BT4	1354	CB25	1388	CF62	1422	BR332
	1321	BW13	1355	CB3	1389	CF78	1423	BR212
	1322	BW18	1356	CB30	1390	CF85	1424	BR195
	1323	BW2	1357	CB37	1391	CF89	1425	BR194
20	1324	BW51	1358	CC144	1392	BR814	1426	BR19
	1325	BW61	1359	CC145	1393	BR782	1427	BR141
	1326	BW83	1360	CC149	1394	BR778	1428	BR122
	1327	BV185	1361	CC153	1395	BR77	1429	BR107
	1328	BV195	1362	CC162	1396	BR767	1430	BR1010
25	1329	BV200	1363	CC25	1397	BR758	1431	BR101
	1330	BV202	1364	CC31	1398	BR733	1432	BR1008
	1331	BV204	1365	CC322	1399	BR719	1433	BQ135
	1332	BV206	1366	CC39	1400	BR711	1434	BP913
	1333	BV210	1367	CC397	1401	BR71	1435	BP911
30	1334	BV212	1368	CC403	1402	BR63	1436	BP897
	1335	BV227	1369	CC46	1403	BR616	1437	BP895
	1336	BV238	1370	CC50	1404	BR610	1438	BP894
	1337	BV239	1371	CC59	1405	BR607	1439	BP893
	1338	BV241	1372	CC69	1406	BR595	1440	BP884

	1441	BP883	1475	BU65
	1442	BP875	1476	BU68
	1443	BP870	1477	BU76
	1444	BP859	1478	BV106
5	1445	BP837	1479	BV112
	1446	BP833	1480	BV123
	1447	BP499	1481	BV124
	1448	BP492	1482	BV126
	1449	BP488	1483	BV128
10	1450	BP484	1484	BV131
	1451	BP483	1485	BV133
	1452	BP481	1486	BV134
	1453	BP475	1487	BV135
	1454	BN418	1488	BV138
15	1455	BN415	1489	BV139
	1456	BN405	1490	BV140
	1457	BN394	1491	BV141
	1458	BN390	1492	BV145
	1459	BN387	1493	BV15
20	1460	BN379	1494	BV158
	1461	BN377	1495	BV160
	1462	BR84	1496	BV172
	1463	BR853	1497	BV180
	1464	BR854	1498	BV21
25	1465	BR884	1499	BV27
	1466	BT160	1500	BV29
	1467	BU165		
	1468	BU29		
	1469	BU44		
30	1470	BU45		
	1471	BU53		
	1472	BU57		
	1473	BU6		
	1474	BU60		

The "Clone ID No." for a particular clone consists of one or two letters followed by a number. The letters designate the tissue source from which the sEST was isolated. Table 3 below lists the various sources which were run through applicants' signal sequence trap. Thus, the tissue source for a particular sEST sequence can be identified in Table 3 by the one and two letter designations used in the relevant "Clone ID No.". For example, a clone designated as "BA312" would have been isolated from a human placenta (26 yrs.) library (i.e., selectin "BA") as indicated in Table 3.

As used herein, "polynucleotide" includes single- and double-stranded RNAs, DNAs and RNA:DNA hybrids.

As used herein a "secreted" protein is one which, when expressed in a suitable host cell, is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins which are transported across the membrane of the endoplasmic reticulum.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H.U. Saragovi, *et al.*, Bio/Technology 10, 773-778 (1992) and in R.S. McDowell, *et al.*, J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites. For example, fragments of the protein may be fused through "linker" sequences to the Fc portion of an immunoglobulin. For a bivalent form of the protein, such a fusion could be to the Fc portion of an IgG molecule. Other immunoglobulin isotypes may also be used to generate such fusions. For example, a protein - IgM fusion would generate a decavalent form of the protein of the invention.

The present invention also provides both full-length and mature forms of the disclosed proteins. The full-length form of the such proteins is identified in the sequence listing by translation of the nucleotide sequence of each disclosed clone. The mature form of such protein may be obtained by expression of the disclosed full-length polynucleotide (preferably those deposited with ATCC) in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein may also be determinable from the amino acid sequence of the full-length form.

The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification  
5 and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials.

Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such forms part or all of the intracellular and transmembrane domains of the protein are deleted such that  
10 the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known techniques for determination of such domains from sequence information.

Species homologs of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making  
15 suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the  
20 polynucleotides disclosed herein.

The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

The present invention also includes polynucleotides capable of hybridizing, preferably under reduced stringency conditions, more preferably under stringent conditions,  
25 most preferably under highly stringent conditions, to polynucleotides described herein. Examples of stringency conditions are shown in Table 1 below: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.



Table 1

	Stringency Condition	Polynucleotide Hybrid	Hybrid Length (bp) <sup>†</sup>	Hybridization Temperature and Buffer <sup>†</sup>	Wash Temperature and Buffer <sup>†</sup>
5	A	DNA:DNA	≥ 50	65°C; 1xSSC -or- 42°C; 1xSSC, 50% formamide	65°C; 0.3xSSC
	B	DNA:DNA	< 50	T <sub>B</sub> *; 1xSSC	T <sub>B</sub> *; 1xSSC
	C	DNA:RNA	≥ 50	67°C; 1xSSC -or- 45°C; 1xSSC, 50% formamide	67°C; 0.3xSSC
	D	DNA:RNA	< 50	T <sub>D</sub> *; 1xSSC	T <sub>D</sub> *; 1xSSC
	E	RNA:RNA	≥ 50	70°C; 1xSSC -or- 50°C; 1xSSC, 50% formamide	70°C; 0.3xSSC
10	F	RNA:RNA	< 50	T <sub>F</sub> *; 1xSSC	T <sub>F</sub> *; 1xSSC
	G	DNA:DNA	≥ 50	65°C; 4xSSC -or- 42°C; 4xSSC, 50% formamide	65°C; 1xSSC
	H	DNA:DNA	< 50	T <sub>H</sub> *; 4xSSC	T <sub>H</sub> *; 4xSSC
	I	DNA:RNA	≥ 50	67°C; 4xSSC -or- 45°C; 4xSSC, 50% formamide	67°C; 1xSSC
	J	DNA:RNA	< 50	T <sub>J</sub> *; 4xSSC	T <sub>J</sub> *; 4xSSC
15	K	RNA:RNA	≥ 50	70°C; 4xSSC -or- 50°C; 4xSSC, 50% formamide	67°C; 1xSSC
	L	RNA:RNA	< 50	T <sub>L</sub> *; 2xSSC	T <sub>L</sub> *; 2xSSC
	M	DNA:DNA	≥ 50	50°C; 4xSSC -or- 40°C; 6xSSC, 50% formamide	50°C; 2xSSC
	N	DNA:DNA	< 50	T <sub>N</sub> *; 6xSSC	T <sub>N</sub> *; 6xSSC
	O	DNA:RNA	≥ 50	55°C; 4xSSC -or- 42°C; 6xSSC, 50% formamide	55°C; 2xSSC
20	P	DNA:RNA	< 50	T <sub>P</sub> *; 6xSSC	T <sub>P</sub> *; 6xSSC
	Q	RNA:RNA	≥ 50	60°C; 4xSSC -or- 45°C; 6xSSC, 50% formamide	60°C; 2xSSC
	R	RNA:RNA	< 50	T <sub>R</sub> *; 4xSSC	T <sub>R</sub> *; 4xSSC

‡: The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

\*: SSPE (1xSSPE is 0.15M NaCl, 10mM NaH<sub>2</sub>PO<sub>4</sub>, and 1.25mM EDTA, pH 7.4) can be substituted for SSC (1xSSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

\*T<sub>B</sub> - T<sub>R</sub>: The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (T<sub>m</sub>) of the hybrid, where T<sub>m</sub> is determined according to the following equations. For hybrids less than 18 base pairs in length, T<sub>m</sub>(°C) = 2(# of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length, T<sub>m</sub>(°C) = 81.5 + 16.6(log [Na<sup>+</sup>]) + 0.41(%G+C) - (600/N), where N is the number of bases in the hybrid, and [Na<sup>+</sup>] is the concentration of sodium ions in the hybridization buffer ([Na<sup>+</sup>] for 1xSSC = 0.165 M).

Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and *Current Protocols in Molecular Biology*, 1995, F.M. Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

Preferably, such hybridizing polynucleotides have at least 70% sequence identity (more preferably, at least 80% identity; most preferably at least 90% or 95% identity) with the polynucleotide of the present invention to which they hybridize, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps. The isolated polynucleotide encoding the protein of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman *et al.*, *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control

sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

5 A number of types of cells may act as suitable host cells for expression of the protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from in vitro culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells.

10 Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any  
15 bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

20 The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *e.g.*, Invitrogen, San Diego, California, U.S.A. (the MaxBac® kit), and such methods are well known in the art,  
25 as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting  
30 expressed protein may then be purified from such culture (i.e., from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl® or Cibacrom blue 3GA

Sepharose®; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX). Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, MA), Pharmacia (Piscataway, NJ) and InVitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("Flag") is commercially available from Kodak (New Haven, CT).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The protein may also be produced by known conventional chemical synthesis. Methods for constructing the proteins of the present invention by synthetic means are known to those skilled in the art. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications in the peptide or DNA sequences can be made by those skilled in the art using known techniques. Modifications

of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Patent No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and may thus be useful for screening or other immunological methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are believed to be encompassed by the present invention.

## USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention  
5 may be provided by administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA).

### Research Uses and Utilities

10 The polynucleotides provided by the present invention can be used by the research community for various purposes. The primary use of polynucleotides of the invention which are sESTs is as probes for the identification and isolation of full-length cDNAs and genomic DNA molecules which correspond (i.e., is a longer polynucleotide sequence of which substantially the entire sEST is a fragment in the case of a full-length cDNA, or  
15 which encodes the sEST in the case of a genomic DNA molecule) to such sESTs. Techniques for use of such sequences as probes for larger cDNAs or genomic molecules are well known in the art.

The polynucleotides can also be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding  
20 protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related  
25 DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-  
30 DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify

polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

#### Nutritional Uses

Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

#### Cytokine and Cell Proliferation/Differentiation Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for T-cell or thymocyte proliferation include without limitation those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., *J. Immunol.* 137:3494-3500, 1986; Bertagnolli et al., *J. Immunol.* 145:1706-1712, 1990; Bertagnolli et al., *Cellular Immunology* 133:327-341, 1991; Bertagnolli, et al., *J. Immunol.* 149:3778-3783, 1992; Bowman et al., *J. Immunol.* 152: 1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A.M. and Shevach, E.M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human Interferon  $\gamma$ , Schreiber, R.D. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., *J. Exp. Med.* 173:1205-1211, 1991; Moreau et al., *Nature* 336:690-692, 1988; Greenberger et al., *Proc. Natl. Acad. Sci. U.S.A.* 80:2931-2938, 1983; Measurement of mouse and human interleukin 6 - Nordan, R. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley



- and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11 - Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9 -
- 5 Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

- Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in:
- 10 *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun.
- 15 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

#### Immune Stimulating or Suppressing Activity

- A protein of the present invention may also exhibit immune stimulating or immune
- 20 suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may
- 25 be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course,
- 30 in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre

syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other  
5 conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune  
10 response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from  
15 immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as , for example, B7)), *e.g.*, preventing  
20 high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys  
25 the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (*e.g.*, B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the  
30 molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-

blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow *et al.*, Science 257:789-792 (1992) and Turka *et al.*, Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosus in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral

infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient  
5 by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro* activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding  
10 a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells *in vivo*.

In another application, up regulation or enhancement of antigen function (preferably  
15 B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (*e.g.*, sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor  
20 cells obtained from a patient can be transfected *ex vivo* with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection  
25 *in vivo*.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or  
30 which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I  $\alpha$  chain protein and  $\beta_2$  microglobulin protein or an MHC class II  $\alpha$  chain protein and an MHC class II  $\beta$  chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I

or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, *Immunologic studies in Humans*); Herrmann et al., *Proc. Natl. Acad. Sci. USA* 78:2488-2492, 1981; Herrmann et al., *J. Immunol.* 128:1968-1974, 1982; Handa et al., *J. Immunol.* 135:1564-1572, 1985; Takai et al., *J. Immunol.* 137:3494-3500, 1986; Takai et al., *J. Immunol.* 140:508-512, 1988; Herrmann et al., *Proc. Natl. Acad. Sci. USA* 78:2488-2492, 1981; Herrmann et al., *J. Immunol.* 128:1968-1974, 1982; Handa et al., *J. Immunol.* 135:1564-1572, 1985; Takai et al., *J. Immunol.* 137:3494-3500, 1986; Bowman et al., *J. Virology* 61:1992-1998; Takai et al., *J. Immunol.* 140:508-512, 1988; Bertagnolli et al., *Cellular Immunology* 133:327-341, 1991; Brown et al., *J. Immunol.* 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, *J. Immunol.* 144:3028-3033, 1990; and Assays for B cell function: *In vitro* antibody production, Mond, J.J. and Brunswick, M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-

3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

#### Hematopoiesis Regulating Activity

A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for

example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet  
 5 transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post  
 10 irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

15 Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. *Cellular Biology* 15:141-151, 1995; Keller et al.,  
 20 *Molecular and Cellular Biology* 13:473-486, 1993; McClanahan et al., *Blood* 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In *Culture of Hematopoietic*  
 25 *Cells*. R.I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., *Proc. Natl. Acad. Sci. USA* 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., *Experimental Hematology* 22:353-359, 1994;  
 30 Cobblestone area forming cell assay, Ploemacher, R.E. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, NY. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland,

H.J. In *Culture of Hematopoietic Cells*. R.I. Freshney, *et al.* eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

#### Tissue Growth Activity

5 A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

10 A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. *De novo* bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma  
15 induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of  
20 progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the  
25 protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein  
30 may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. *De novo* tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic



plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured  
5 by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium ).

10 Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

#### 15 Activin/Inhibin Activity

A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention,  
20 alone or in heterodimers with a member of the inhibin  $\alpha$  family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- $\beta$  group, may  
25 be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

30 The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale

et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

#### Chemotactic/Chemokinetic Activity

5 A protein of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide  
10 particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can  
15 stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

20 The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one  
25 cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et  
30 al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25: 1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

#### Hemostatic and Thrombolytic Activity

A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

10        Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., *J. Clin. Pharmacol.* 26:131-140, 1986; Burdick et al., *Thrombosis Res.* 45:413-419, 1987; Humphrey et al., *Fibrinolysis* 5:71-79 (1991); Schaub, *Prostaglandins* 35:467-474, 1988.

15        Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction.

25        A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: *Current Protocols in Immunology*, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., *Proc. Natl. Acad. Sci. USA* 84:6864-6868, 1987; Bierer et al., *J. Exp. Med.* 168:1145-1156, 1988; Rosenstein et al., *J. Exp. Med.*

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169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

#### Anti-Inflammatory Activity

5 Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or  
10 suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality,  
15 arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

#### Tumor Inhibition Activity

20 In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor  
25 precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

#### Other Activities

30 A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting

(suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

20

## ADMINISTRATION AND DOSING

A protein of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources) may be used in a pharmaceutical composition when combined with a pharmaceutically acceptable carrier. Such a composition may also contain (in addition to protein and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or compliment its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein of the invention, or to minimize side effects. Conversely, protein of the present invention may be included in formulations of the particular cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent.

A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that

can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

5           The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, 10 diglycerides, sulfatides, lysolecithin, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent No. 4,235,871; U.S. Patent No. 4,501,728; U.S. Patent No. 4,837,028; and U.S. Patent No. 4,737,323, all of which are incorporated herein by reference.

15           As used herein, the term "therapeutically effective amount" means the total amount of each active component of the pharmaceutical composition or method that is sufficient to show a meaningful patient benefit, i.e., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, 20 administered alone, the term refers to that ingredient alone. When applied to a combination, the term refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

          In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein of the present invention is administered to a 25 mammal having a condition to be treated. Protein of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein of the present invention may be administered either 30 simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.



Administration of protein of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous  
5 administration to the patient is preferred.

When a therapeutically effective amount of protein of the present invention is administered orally, protein of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an  
10 adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein of the present invention, and preferably from about 25 to 90% protein of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain  
15 physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein of the present invention, and preferably from about 1 to 50% protein of the present invention.

20 When a therapeutically effective amount of protein of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical  
25 composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers,  
30 antioxidants, or other additives known to those of skill in the art.

The amount of protein of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein of the present invention with

which to treat each individual patient. Initially, the attending physician will administer low doses of protein of the present invention and observe the patient's response. Larger doses of protein of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01  $\mu$ g to about 100 mg (preferably about 0.1 mg to about 10 mg, more preferably about 0.1  $\mu$ g to about 1 mg) of protein of the present invention per kg body weight.

The duration of intravenous therapy using the pharmaceutical composition of the present invention will vary, depending on the severity of the disease being treated and the condition and potential idiosyncratic response of each individual patient. It is contemplated that the duration of each application of the protein of the present invention will be in the range of 12 to 24 hours of continuous intravenous administration. Ultimately the attending physician will decide on the appropriate duration of intravenous therapy using the pharmaceutical composition of the present invention.

Protein of the invention may also be used to immunize animals to obtain polyclonal and monoclonal antibodies which specifically react with the protein. Such antibodies may be obtained using either the entire protein or fragments thereof as an immunogen. The peptide immunogens additionally may contain a cysteine residue at the carboxyl terminus, and are conjugated to a hapten such as keyhole limpet hemocyanin (KLH). Methods for synthesizing such peptides are known in the art, for example, as in R.P. Merrifield, J. Amer.Chem.Soc. 85, 2149-2154 (1963); J.L. Krstenansky, *et al.*, FEBS Lett. 211, 10 (1987). Monoclonal antibodies binding to the protein of the invention may be useful diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal antibodies binding to the protein may also be useful therapeutics for both conditions associated with the protein and also in the treatment of some forms of cancer where abnormal expression of the protein is involved. In the case of cancerous cells or leukemic cells, neutralizing monoclonal antibodies against the protein may be useful in detecting and preventing the metastatic spread of the cancerous cells, which may be mediated by the protein.

For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a

pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein of the invention which may also  
5 optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and  
10 cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices  
15 for the compositions may be biodegradable and chemically defined calcium sulfate, tricalciumphosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such  
20 as sintered hydroxapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalciumphosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability.

25 Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

30 A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate,

poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt%, preferably 1-10 wt% based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells.

In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- $\alpha$  and TGF- $\beta$ ), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins of the present invention.

The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA).

Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

Patent and literature references cited herein are incorporated by reference as if fully set forth.

Table 3

Sel.	Species	Tissue	Cell Type
AA	Human	Kidney	19-23wks., M/F pool of 5
AB	Human	Fetal Lung	Fetal Lung
AC	Human	Placenta	26yrs., 1 specimen
AD	Murine	Embryo	Fetal ES cells
AE	Murine	Spleen	Adult spleen
AF	Murine	Fetal Brain	Fetal Brain
AG	Murine	Fetal Brain	Fetal Brain
AH	Murine	Fetal Thymus	Fetal Thymus
AI	Human	Blood	Adult PBMC/TH1or2
AJ	Human	Testes	10-61yrs., pool of 11
AK	Human	Kidney	19-23wks., M/F pool of 5
AL	Human	Neural	Adult Glioblastoma line TG-1
AM	Human	Kidney	19-23wks., M/F pool of 5
AN	Murine	Bone Marrow	Adult Stromal cell line FCM-4
AO	Murine	Thymus	Adult Subtr. Adult Thymus
AP	Human	Placenta	26yrs., 1 specimen
AQ	Human	Ovary	PA-1 Teratocarcinoma
AR	Human	Retina	16-75yrs., pool of 76
AS	Human	Brain	19-23wks., M/F pool of 5
AT	Human	Blood	Adult lymphocytes+dend. cells
AU	Human	Testes	10-61yrs., pool of 11
AV	Murine	Spleen	Adult spleen
AW	Human	Ovary	PA-1 Teratocarcinoma
AX	Human	Testes	10-61yrs., pool of 11
AY	Human	Retina	16-75yrs., pool of 76
AZ	Human	Colon	Caco-2 Adenocarcinoma
B	Human	Blood	PeripheralBloodMononuclearCell
BA	Human	Placenta	26yrs., 1 specimen
BB	Human	Blood	Adult PBMC/TH1or2
BC	Murine	Embryo	Fetal ES cells
BD	Human	Kidney	19-23wks., M/F pool of 5
BE	Human	Blood	Adult PBMC/TH1or2
BF	Human	Brain	19-23wks., M/F pool of 5
BG	Human	Brain	N/A
BH	Human	Ovary	PA-1 Teratocarcinoma
BI	Human	Kidney	19-23wks., M/F pool of 5
BJ	Human	Ovary	PA-1 Teratocarcinoma
BK	Human	Retina	16-75yrs., pool of 76
BL	Human	Testes	10-61yrs., pool of 11
BM	Human	Muscle	N/A
BN	Human	Placenta	26yrs., 1 specimen
BO	Human	Retina	16-75yrs., pool of 76
BP	Human	Kidney	19-23wks., M/F pool of 5
BQ	Human	Colon	Caco-2 Adenocarcinoma Caco2

BR	Human	Kidney	19-23wks., M/F pool of 5
BS	Human	Pituitary	Adult Pituitary
BT	Human	Blood	Adult PBMC
BU	Human	Placenta	26yrs., 1 specimen
BV	Human	Brain	N/A
BW	Human	Blood	Adult PBMC
BX	Human	Ovary	PA-1 Teratocarcinoma
BY	Human	Blood	Adult PBMC/TH1or2
BZ	Human	Kidney	19-23wks., M/F pool of 5
C	Human	Blood	PeripheralBloodMononuclearCell
CA	Murine	Embryo	Fetal ES cell embryoid bodies
CB	Human	Brain	19-23wks., M/F pool of 5
CC	Human	Brain	N/A
CD	Human	Brain	19-23wks., M/F pool of 5
CE	Human	Blood	Adult lymphocytes+dend. cells
CF	Human	Placenta	26yrs., 1 specimen
CG	Human	Testes	10-61yrs., pool of 11
CH	Human	Kidney	19-23wks., M/F pool of 5
CI	Human	Brain	N/A
CJ	Human	Brain	19-23wks., M/F pool of 5
CK	Human	Testes	10-61yrs., pool of 11
CL	Human	Retina	16-75yrs., pool of 76
CM	Human	Adult Lung	Adult Lung
CN	Human	Brain	19-23wks., M/F pool of 5
CO	Human	Brain	N/A
CP	Human	SalivaryGland	N/A
CQ	Human	Heart	13-73yrs., pool of 3
CR	Human	Testes	10-61yrs., pool of 11
CS	Human	Brain	19-23wks., M/F pool of 5
CT	Human	Brain	N/A
CU	Human	Pineal Gland	N/A
CV	Human	Mammary	Adult Human Mammary
CW	Human	Brain	19-23wks., M/F pool of 5
CY	Human	Pineal Gland	N/A
CZ	Human	Testes	10-61yrs., pool of 11
D	Human	Blood	PeripheralBloodMononuclearCell
DA	Human	Placenta	26yrs., 1 specimen
DB	Human	Prostate	Adult Prostate
DC	Human	Pineal Gland	Adult Pineal Gland
DD	Human	Testes	10-61yrs., pool of 11
DE	Human	Testes	Adult NCCIT TeratoCA
DF	Human	Brain	N/A
DG	Human	Placenta	26yrs., 1 specimen
DH	Human	Brain	19-23wks., M/F pool of 5
DI	Human	Testes	10-61yrs., pool of 11
DJ	Human	Placenta	26yrs., 1 specimen
DK	Human	Fetal Kidney2	Fetal Kidney

DL	Human	Brain	N/A
DM	Human	Brain	N/A
DN	Human	Brain	19-23wks., M/F pool of 5
DO	Human	Testes	10-61yrs., pool of 11
DP	Murine	Embryo	Fetal ES cell embryoid bodies
DQ	Human	Placenta	26yrs., 1 specimen
DR	Human	SalivaryGland	N/A
DT	Human	Brain	N/A
DU	Human	Brain	19-23wks., M/F pool of 5
DV	Human	Pineal Gland	Adult Pineal Gland
DW	Human	Brain	N/A
DX	Human	Testes	10-61yrs., pool of 11
DY	Human	Brain	N/A
DZ	Human	Testes	Adult NCCIT TeratoCA
E	Human	Blood	PeripheralBloodMononuclearCell
EA	Human	Brain	19-23wks., M/F pool of 5
EB	Human	Melanoma	Adult Melanoma
EC	Human	Brain	N/A
ED	Human	Placenta	26yrs., 1 specimen
EE	Human	Testes	10-61yrs., pool of 11
EF	Human	Liver	Adult Liver
EG	Human	Pancreas	Adult HPC-3 Ductal AdenoCA
EH	Human	Blood	PeripheralBloodMononuclearCell
EI	Human	Brain	19-23wks., M/F pool of 5
EJ	Human	Placenta	26yrs., 1 specimen
EK	Human	Brain	19-23wks., M/F pool of 5
EL	Human	Testes	10-61yrs., pool of 11
EM	Human	Fetal Kidney2	Fetal Kidney
EN	Human	Brain	19-23wks., M/F pool of 5
EO	Human	Adrenal Gland	Adult Adrenal Gland
EP	Human	Placenta	26yrs., 1 specimen
EQ	Human	Testes	10-61yrs., pool of 11
ER	Human	Brain	19-23wks., M/F pool of 5
ES	Human	Placenta	26yrs., 1 specimen
ET	Human	Testes	10-61yrs., pool of 11
EU	Human	Kidney	Adult Kidney
EV	Human	Stomach	Adult Stomach
EW	Human	Placenta	26yrs., 1 specimen
EX	Human	Testes	10-61yrs., pool of 11
EY	Human	Brain	19-23wks., M/F pool of 5
EZ	Human	Fetal Kidney2	Fetal Kidney
FA	Human	Brain	19-23wks., M/F pool of 5
FB	Human	Placenta	26yrs., 1 specimen
FC	Human	Testes	10-61yrs., pool of 11
FD	Human	SalivaryGland	N/A
FE	Human	Brain	N/A
FF	Human	Testes	Adult NCCIT TeratoCA



FG	Human	Brain	N/A
FH	Human	Brain	19-23wks., M/F pool of 5
FI	Human	Small Intest	Adult Small Intestine
FJ	Human	Lung CA	Adult Lung CA
FK	Human	Kidney	Adult Kidney
FM	Human	Brain	N/A
FN	Human	Brain	19-23wks., M/F pool of 5
FO	Human	Brain	N/A
FP	Human	Placenta	26yrs., 1 specimen
FQ	Human	Testes	10-61yrs., pool of 11
FR	Human	Placenta	26yrs., 1 specimen
FS	Human	Testes	10-61yrs., pool of 11
FT	Chicken	Fetal Lung	Fetal Lung
FU	Chicken	Limb Bud	Fetal St. 23 Limb Bud
FV	Human	Testes	Adult NCCIT TeratoCA
FW	Human	Testes	Adult NCCIT TeratoCA
FX	Human	Brain	19-23wks., M/F pool of 5
FY	Human	Placenta	26yrs., 1 specimen
FZ	Human	Placenta	26yrs., 1 specimen
G	Human	Blood	PeripheralBloodMononuclearCell
GA	Human	Testes	10-61yrs., pool of 11
GB	Human	Placenta	26yrs., 1 specimen
GC	Human	Testes	10-61yrs., pool of 11
GD	Human	Placenta	26yrs., 1 specimen
GE	Human	Brain	N/A
GF	Human	Brain	19-23wks., M/F pool of 5
GG	Human	Fetal Kidney2	Fetal Kidney
GH	Human	Placenta	26yrs., 1 specimen
GI	Human	Retinoblastoma	Adult Retinoblastoma Y79
GJ	Murine	Spleen	Adult Spleen
GK	Human	Fetal Kidney2	Fetal Kidney
GL	Murine	Lymph Node	Adult Lymph Node
GM	Human	Uterus	N/A
GN	Human	Blood	PeripheralBloodMononuclearCell
GO	Human	Adrenal Gland	Adult Adrenal Gland
GP	Human	Ovary	PA-1 Teratocarcinoma
GQ	Human	Pineal Gland	N/A
GR	Human	Pancreas	Adult HPC-3 Ductal AdenoCA
GS	Human	Retina	16-75yrs., pool of 76
GT	Human	Brain	N/A
GU	Human	Fetal Kidney2	Fetal Kidney
GV	Rat	Retina	Newborn Retina
GW	Chicken	Limb Bud	Fetal St.26 Limb Bud
GX	Human	Brain	N/A
GY	Human	Testes	10-61yrs., pool of 11
GZ	Human	Brain	19-23wks., M/F pool of 5
H	Human	Blood	PeripheralBloodMononuclearCell

HA	Human	Testes	Adult NCCIT TeratoCA
HB	Human	Fetal Kidney2	Fetal Kidney
HC	Human	Brain	19-23wks., M/F pool of 5
HD	Human	Brain	N/A
HE	Human	Testes	10-61yrs., pool of 11
HF	Human	Brain	19-23wks., M/F pool of 5
HG	Human	Fetal Kidney2	Fetal Kidney
HH	Human	Brain	N/A
HI	Human	Testes	10-61yrs., pool of 11
HJ	Human	Brain	N/A
HK	Human	Brain	19-23wks., M/F pool of 5
HL	Human	Fetal Kidney2	Fetal Kidney
HM	Human	Testes	Adult NCCIT TeratoCA
HN	Human	Fetal Kidney2	Fetal Kidney
HO	Human	Brain	N/A
HP	Human	Brain	19-23wks., M/F pool of 5
HQ	Human	Testes	10-61yrs., pool of 11
HR	Human	Brain	N/A
HS	Human	Brain	N/A
HT	Human	Brain	19-23wks., M/F pool of 5
HU	Human	Fetal Kidney2	Fetal Kidney
HV	Human	Testes	10-61yrs., pool of 11
HW	Human	Brain	N/A
HX	Human	Brain Hippoca	Adult Brain Hippocampus
HY	Human	Trachea	Adult Trachea
HZ	Human	Brain Thalamus	Adult Brain Thalamus
I	Human	Blood	PeripheralBloodMononuclearCell
IA	Human	Thyroid	Adult Thyroid
IB	Human	Embryonal CA	Fetal NT2-D1
IC	Human	WER1-Rb1 line	Adult Retinoblastoma
ID	Human	Muscle	N/A
IE	Human	Brain	19-23wks., M/F pool of 5
IF	Human	Uterus	N/A
IG	Human	Testes	10-61yrs., pool of 11
IH	Human	Muscle	N/A
II	Human	Brain	N/A
IJ	Human	Blood	PeripheralBloodMononuclearCell
IK	Human	Retinoblastoma	Adult Retinoblastoma Y79
IL	Human	Retina	16-75yrs., pool of 76
IM	Human	Various	Various
IN	Human	Prostate	Adult Prostate
IO	Human	Brain	19-23wks., M/F pool of 5
IP	Human	Fetal Kidney2	Fetal Kidney
IQ	Human	Prostate	Adult Prostate
IR	Human	Brain Hippoca	Adult Brain Hippocampus
IS	Human	Trachea	Adult Trachea
IT	Human	Brain Thalamu	Adult Brain Thalamus

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Jacobs, Kenneth  
McCoy, John  
LaVallie, Edward  
Racie, Lisa  
Merberg, David  
Treacy, Maurice  
Spaulding, Vikki  
Agostino, Michael
- (ii) TITLE OF INVENTION: SECRETED, EXPRESSED SEQUENCE TAGS
- (iii) NUMBER OF SEQUENCES: 1500
- (iv) CORRESPONDENCE ADDRESS
  - (A) ADDRESSE: Genetics Institute, Inc.
  - (B) STREET: 87 CambridgePark Drive
  - (C) CITY: Cambridge
  - (D) STATE: Massachusetts
  - (E) COUNTRY: U.S.A
  - (F) ZIP: 02140
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy Disk
  - (B) COMPUTER: IBM PC Compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (vii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Brown, Scott A.
  - (B) REGISTRATION NUMBER: 32,724
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (617) 498-8224
  - (B) TELEFAX: (617) 876-5851

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 335 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTGACCCCA TCCCATCCAA TAGTCCCAT CTCTCTCAG CTCTCTCTGT AGTTTCTCTT	60
CCTCCGCCTG CCTTTTAACT TAGTGTTTCC CAGGACAGAG GTGACTCAGT TGTATCCAGA	120
CCGCTCTGTG ACTGAACACC CACTTCTTTT TCCTTTTCCA ATAAATATAT GTAACATACA	180
TGTCAACTAG GAACAAAACA GTATCTCAGG AATCCACCAT CCAGTAAAA ATGGACCCTT	240

ACCCTTACCG TGCCCTGCA GAGACCCCAA TACAGCGCAT TTCCCTCATF CTTTGCTTT	300
TCTCAAGTTT TACCACGGCC TCTTGGCCC TCGAG	335

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAATTCGGCC AAAGAGGCCG TTGACCATTG ATAGAACACA GGCATACACA GGAAGATACA	60
TTCACAGAAG AGCTTCCTGC ACAAAGTAAG CCACCAGCGC AACATGACAG TGAAGACCCCT	120
GCATGCCCCA GCCATGGTCA AGTACTTGCT GCTGTCGATA TTGGGGCTTG CTTTCTGAG	180
TGAGGCGGCA GCTCGGAAAA TCCCCAAAGT AGGACATACT TTTTCCAAA AGCCTGAGAG	240
TTGCCCCGCT GTGCCAGGAG GTAGTATGAA GCTTGACATT GGCATCATCA ATGAAAACCA	300
GCGCGTTTCC ATGTACGTA ACATCGAGAG CCGCTCCACC TCCCCCTGGA ATTACACTGT	360
CACTTGGGAC CCCAACCGGT ACCCTCGGA AGTTGTACAG GCCCAGTGTA GGAACCTGGG	420
CTGCATCAAT GCTCAAGGAA AGGAAGACAT CTCCATGAAT TCCGTTCCCA TCCAGCAAGA	480
GACCCTGTCG ACGGCCTCTT TGGCCCTCGA GACA	514

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTGACCCCTC CACCTGCAAA TCCACTGTCC ATACCCTTGG ATTGGTTGAA GAGCCTTTGG	60
TCATACTGAA CTTATTGGA AGTCCGAGGA TTAGGAACAC CGAGAGCAAT AACTTCACTG	120
ATATCCCGAT TTTCATTTCT CTGAAGTTTC GACCTCTTAT CAGGAGCTGC CCTGGAAAGA	180
TTCCGGTCAT GCTGTCTCTC TTTTCGCCTG TCATGCCGGA TTTTCATCCCT CTCACGTGCC	240
TCCCCATCCT CTTTTTCCAC ATGAGTTTGG ATCCAGCTC TTCTCTCCCT GGCTTTCTGG	300
GCCATTTCTC TAAGTTTCTC TNCANGTNTN NCCTTTTCTT TCTGAGCCAT TTTTCTCTCT	360
ACTTGGGCGT CGACGGCCTC TGGGGCCCTC GAG	393

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTGACCCAGG CATAACAGG AAGATACATT CACAGAAAGA GCTTCCTGCA CAAAGTAAGC	60
CACCAGCGCA ACATGACAGT GAAGACCCTG CATGGCCAG CCATGGTCAA GTACTTGCTG	120

CTGTCGATAT TGGGGCTTGC CTTTCTGAGT GAGGCGGCAG CTCGGAAAAT CCCCCAAGTA	180
GGACATACTT TTTTCCAAAA GCCTGAGAGT TGCCCGCCTG TGCCAGGAGG TAGTATGAAG	240
CTTGACATTG GCATCATCAA TGAACCAG CGCGTTTCCA TGTCACGTAA CATCGAGAGC	300
CGCTCCACCT CCCCCTGGAA TTACACTGTC ACTTGGGACC CCAACCGGTA CCCCTCGGAA	360
GTTGTACAGG CCCAGTGTAG GAACTTGGGC TGATCAATG CTCAAGGAAA GGAAGACATC	420
TCCATGAATT CCGTTCCCAT CCAGCAAGAG ACCCTGGTCG TCCGGAGGAA GCACCAAGGC	480
TGCTCTGTTT CTTTCCAGTT GGAGAAGGTG CTGGTGACTG TTGGCTGCAC CTGCGTCACG	540
TCAACGGCCT CTTTGGCCCT CGAG	564

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTCGACCTTC AGTTGCCTCA GACCCAGTA ATACAACGGT CACCACCATG AAACCTACAG	60
CGGCATCTAA TACAACAACA CCAGGGATGG TCTCAACAAA TATGACTTCT ACCACCTTAA	120
AGTCTACACC CAAAACAACA AGTGTTTCAC AGAACACATC TCAGATATCA ACATCCACAA	180
TGACCGTAAC CCACAATAGT TCAGTGACAT CTGTGCTTC ATCAGTAACA ATCACAACAA	240
CTATGCATTG TGAAGCAAAG AAAGGATCAA AATTGATAC TGGGAGCTTT GTTGGTGGTA	300
TTGTATTAAAC GCTGGGAGTT TTATCTATTC TGTCACGGC CTCTTTGGCC CTCGAG	356

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 520 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTA CTGCTGC ACGGACTCTG GAACCATGAA CATATTTGAT CGAAAGATCA ACTTTGATGC	60
GCTTTTAAAA TTTTCTCATA TAACCCCGTC AACGCAGCAG CACCTGAAGA AGGTCTATGC	120
AAGTTTGGCC CTTTGTATGT TTGCGGCGGC TGCAGGGGCC TATGTCCATA TGGTCACTCA	180
TTTCATTGAG GCTGGCCTGC TGTCTGCCTT GGGCTCCCTG ATATTGATGA TTTGGCTGAT	240
GGCAACACCT CATAGCCATG AAAGTGAACA GAAAAGACTG GGA CTCTCTTG CTGGATTGTC	300
ATTCCTTACA GGAGTTGGCC TGGGCCCTGC CTTGGAGTTT TGTATTGCTG TCAACCCAG	360
CATCCTTCCC ACTGCTTTCA TGGGCACGGC AATGATCTTT ACCTGCTTCA CCCTCAGTGC	420
ACTCTATGCC AGGCGCCGCG GCTACCTCTT TCTGGGAGGT ATCTTGATGT CAGCCCTGAG	480
CTTGTTGCTT TTGTCGACGG CCTCTTTGGC CCTCGAGACA	520

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTCGACGTAC	CACCAGCAAC	CATCAATCCC	GTCTCCTCCT	GCCTCCTCTC	CTGCAATCCA	60
CCCCGCCACG	ACTATCGCCA	TGGCAGCCCT	GATCGCAGAG	AACTTCCGCT	TCCTGTCACT	120
TTTCTTCAAG	AGCAAGGATG	TGATGATTTT	CAACGGCCTG	GTGGCACTGG	GCACGGTGGG	180
CAGCCAGGAG	CTGTCTCTCTG	TGGTGGCCTT	CCACTGCCCC	TGCTCGCCGG	CCCGGAACATA	240
CCTGTACGGG	CTGGCGGCCA	TCGGCGTGCC	CGCCCTGGTG	CTCTTCATCA	TTGGCATCAT	300
CCTCAACAAC	CACACCTGGA	ACCTCGTGGG	CGAGTGCCAG	CACCGGAGGA	CCAAGAACTG	360
CTCCGCCGCC	CCCACCTTCC	TCCTTCTAAG	CTCCATCCTG	GGACGTGCGG	CTGTGGCCCC	420
TGTCACCTGG	TCTGTCTATCT	CCCTGCTGCG	TGGTGAGGCT	TATGTCTGTG	CTCTCAGTGA	480
GTTCTGTGGAC	CCTTCCTCAC	TCACGGCCTC	TTTGGCCCTC	GAGACA		526

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTCAMCTGTG	CAGCGGAGTT	TGACTTTATG	GAAAAAGAGA	CTCCACTGAG	ATACACAAAG	60
ACATTATTGC	TTCCAGTTGT	TCTTGTAGTG	TTTGTGCTA	TTGTTAGAAA	GATTATTAGT	120
GATATGTGGG	GTGTCTTAGC	TAAACAACAG	ACACATGTAA	GAAAACACCA	GTTTGATCAT	180
GGAGAGCTGG	TTTACCATGC	ATTGCAATTG	TTAGCATATA	CAGCCCTTGG	TATTTTAATT	240
ATGAGACTAA	AACTCTTCTT	GACACCATAC	ATGTGTGTTA	TGGCATCACT	GATCTGCTCA	300
AGACAGCTAT	TTGGATGGCT	CTTTTGCAAA	GTACATCCTG	GTGCTATTGT	GTTTGTATATA	360
TTAGCAGCAA	TGTCAATACA	AGGTTGAGCA	AATCTGCAAA	CCCAGTGGAA	GTCGACGGCC	420
TCTTTGGCCC	TCGAGACA					438

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTCGACCCTA	CACCATGTTT	TTCTCCACGT	TCTACCACGC	CTGCGACCAG	CCCGGGGAGG	60
CGGTGCTGTG	CATCCTCAGC	TACGACACGC	TGCAGTACTG	CGACTTCTTG	GGCTCCGGGG	120
CGGCCATCTG	GGTCACCATC	CTGTGCATGG	CACGGCTCAA	GACAGCCCTG	AAATACGTGC	180
TGTTTCTTCT	GGGTACACTG	GTCATCGCCA	TGTCCTTGCA	GCTGGACCGC	AGGGGCATGT	240
GGAACATGCT	GGGGCCCTGC	CTCTTTGCCT	TCGTGATCAT	GGCCTCCATG	TGGGCTTACC	300
GCTGCGGGCA	CCGGCGCCAG	TGCTACCCCA	CCTCGTGGCA	GCGCTGGGCC	TTCTACCTCC	360
TGCCCCGGCT	CTCTACGGCC	TCTTTGGCCC	TCGAG			395

## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTCGACAGAM WNCAACCCTC AGACGCCACA TCCCCTKACA AGCTGMCAGG CAGGTTCTCT	60
TCCTCTCACA TACTGACCCA CGGKTCCACC CTCTCTCCCC TGGAAAGGAC ACCATGAGCA	120
CTGAAAGCAT GATCCGGRAC GTGGAGCTGK CCGAGGAGGN GYTCCCCAAG AAGACAGGGG	180
GGRCCCAGGG CTCCAGGCGG GGGTTTGTTT CTCAGWCTCT TCTCCTTCCT GATCGNGGGA	240
GGGGGCACCA CGCTCTTCTG TCTGCTGGAC TTTGGAGTGA TCGNCCCCA GAGGGAAGGA	300
GTCCCCCAGG GGAACCTCTC T	321

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 532 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GTCGACGGCC GAGAWGGACA TGAAGCAATA TCAAGGCTCC GCGGGCGTCG CCATGGATGT	60
GGNACGGAGT CGTTTCCCCT ACTGCGTGGT GTGGACGCCC ATCCCGGTGN TCACGTGGTT	120
TTTCCCCATC ATCGGCCACA TGGGCATCTG CACATCCACA GGAGTCATTC GGGACTTCGC	180
GGGCCCCCTAC TTTGTCTCAG AGGACAACAT GGCTTTTGA AAGCCTGCCA AGTACTGGAA	240
GTTGGACCCT GCTCAGGTCT ATGCTAGCGG GCCCAACGCA TGGGACACGG CTGTGCACGA	300
CGCCTCTGAG GAGWACAAGC ACCGCATGCA CAATCTCTGC TGTGACAACT GCCACTCGCA	360
CGTGGCATCG GCCCTGAATC TGATGCGCTA CAACAACAGC ACCAACTGGA ATATGGTGAC	420
GCTCTGCTTC TTCTGCTGCT TCTACGGGAA GTACGTCAGC GTTGGGGCCT TCCTGAAGAC	480
CTGGCTGCCC TTCATCCTTC TCCTGTCGAC GGCCTCTTTG GCCCTCGAGA CA	532

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTGTACACCA AGATGATGAC CAAGAAGCCG GGCATGTTCT TCAACCCCGA GGAGTCGGAG	60
CTGGACCTGA CCTACGGNAA CAGATACAA NACGTGAAGC TCCCTGACGN CTACGAGCGC	120
CTCATCCTGG ACGTCTTCTT TGGGAGGCAG ATGNACTTCG TGCGCAGGGA CGANCTCCNT	180
GAGGNCTGGC GTATTTTTC A CCCCCTGNT GTACCANATT GAGCTNGAGA AGGCCAAGCC	240
TCCAGGAACA CATGTGGGGT CATTACCAAA CAGGGTCCAT CCACATGATG GTGAACATCA	300
ANCTTTGGGC GGACAANGAT TGCTGGGAAT GGGAACTCTG TTCACTGGGG AGCTCTGGGA	360
GTTCTTGAGC TTTGCTGAAA GGTACCCTGC CATCATCTAT AACATCCTGC TCTTTGGGCT	420
GACCAATGCC CTGGGTCAGA GCWTCATCTT TATGACGATT GTGTATCTTG GTCCCCTGAC	480
CTGCTCCATC ATCACTACAA CTCGAAAGTT CTTCAAAAW KTGCCCGCTG TGATCCTCTT	540
CGCCAATCCC ATGTCGACGG CCTCTTTGGC CCTCGAGACA	580

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 434 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```

GTCGACACTA CTTATGCGGC TACTTTGTCC AGGGCACAAA ATGCCGTGGC AGTATCTAAC      60
TAAACCCCCA CAAACTGCT TAATAACAGT TTKGRATGTG AGAAATTAG ATAATTTAAA      120
TATAAGGTGC AGGTTTAAAT TTCTGAGTTT CTTCTTTTCT ATTTTATTA AAAAGAAAAT      180
AATTTTCAGA TTTAATTGAA TTGGAAGAAA CAATACTTCC CACCAGAAAT ATATATCCTG      240
AAAATTGTAT TTTTGTATA TAAACAACTT TTAAGAAAGA TCATTATCCT TTTCTCTACC      300
TAAATATGAG GAGTCTTAGC ATAATGACAA ATATTATATA TTTTCAATT AATGGTACTT      360
GCTGGATCCA CACTAACATC TTGCTAATA ATCTCATTGT TTCTTCGTCA ACGGCCTCTT      420
TGGCCCTCGA GACA                                     434
  
```

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 523 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```

GTGGACGTTT TTTTTTCTT TTTCTTTTTT TTAAGAAAAA CCCATTTTTT TCCTTAAGGA      60
CTTACTAGCC AAAATTTCTT AAACCTCGAG GACTCTACTA GCCATGGCCG AGCCATTCTT      120
GTCAGAAATAT CAACACCAGC CTCAAAC TAG CAACTGTACA GGTGCTGCTG CTGTCCAGGA      180
AGAGCTGAAC CCTGAGCGCC CCCCAGGCGC GGAGGAGCGG GTGCCCGAGG AGGACAGTAG      240
GTGGCAATCG AGAGCGTTCC CCCAGTTGGG TGGCCGTCCG GGGCCGAGG GGGGAAGGGAG      300
CCTGGAATCC CAACACCTC CCTTGCAGAC CCAGGCCTGT CCAGAATCTA GCTGCCTGAG      360
AGAGGGCGAG AAGGGCCAGA ATGGGGACGA CTCGTCCGCT GCGGCGGACT TYCCGCCGCC      420
GGCAGAAAGTG GAACCGACGC CCGAGGCCGA GCTGCTCGCC CAGCCTTGTC ATGACTCCGA      480
GGCCAGTAAG ATGGGGTCTG CGGCCTCTTT GGCCCTCGAG ACA                          523
  
```

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 142 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```

GTCGACCCTC ANTGTTCTGG AACTGGTCTT GGAAGGGATN GTTTATNCTG AGTACACCTG      60
GGAAGTATTT GGGTACTGTC ANGAGCTGGA GTTGNCTNG NATTACNCTC TTCTGCCNA      120
TCTGGTGGTA GGGGTAAACC NG                                     142
  
```

(2) INFORMATION FOR SEQ ID NO:16:



- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 534 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

GTCCACCCGG GCCGCCCTC GCCGCCGGG CTCTTCGCGG GCTGCTCTTT GTCTCCCCGA      60
CCTCGATCCC TGCCTCTCCG GCGGCGTGCG GGCTCGTCTG AGGCTTCCCG CATCTCCCCG      120
CTGGAAGTCC TGCCTCCCGG GGGTTAGAGG AGGTTTCGTT CGAGGGCTGG AAGCGGGAAA      180
GCGGGGCGGA AGGACTGGGC TCATCGCCTC CTGATTAAGT CGTTGTCTTT ACTTAAAATG      240
ACTTTTCCCC CACTTTGTCA AACTTGAGAA CTGTSTTGTG TGTGTGTGTT TCCTTGAGTC      300
TCTAGCTTCA AAATTAAGAG TAGGCGCTAC CGCTGCGATT GTGGGCAGTT GTGTGGTTGG      360
CGGCTGCGTT TGGAGCTCTG AGTTGAAAAG ATGTACGTGA ATGTATGGTT TAGATTTTGT      420
TCTTTTTTTT GCGATTGTCr GATTGGGAGT ACTTTTCCTT TCGGAAATGG GCGAATTTGG      480
TTTTCTTTT GTTCATTGAG AACTGGGTCT ACGGCCTCTT TGGCCCTCGA GACA              534
  
```

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 558 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```

GTTCMCGAAG GGAAGAAGAA GATGAACAAG AACAATGCCA AGGCTCTGAG CACCTTGCGT      60
CAGAAGATCC GAAAATACAA CCGTGATTTC GAGTCCCATA TCACAAGCTA CAAGCAGAAC      120
CCCGAGCAGT CTGCGGATGA AGATGCTGAG AAAAGTGAGG AGGATTCAGA AGGCTCTTCA      180
GATGTGGATG AGGATGAGGA CGGAGTCAGT GCTGCAACTT TCTTGAAGAA GAAATCAGAA      240
GCTCCTTCTG GGGAGAGTCG CAAATTCCCTC MAAAAGATGG ATGATGAAGA TGAGGACTCA      300
GAAGATTCCG TAGATGATGA AGACTGGGAC WCAGGTTCCA CATCTCCGA CTCCGACTCA      360
GAGGAGGAAG AAGGGAAACA AACCGCGCTG GCCTCAAGAT TTCTTAAAAA GGCACCCACC      420
ACAGATGAGG ACAAGAAGGC AGCCGAGAAG AAACGGGAGG ACAAAGCTAA GAAGAAGCAC      480
GACAGGAAAT CCAAGCGCCT GGATGAGGAG GAGGAGGACA ATGAAGGCGG GGTACCGGCC      540
TCTTTGGCCC TCGAGACA              558
  
```

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 465 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```

GTTGACGGCC AGCTTGCTGT CTAACTTTTC ACATCGGAGA AGCTCCTTGG CCTGGGAGGA      60
CTTCTCCGTG CCTTCCCCCT TCCCAGAGAT GCCCCTGTCT AGGGAGTGGC AGAGACCATC      120
CTGGAGGGTG CCAGGAGCGG GGGCCCGTCT GAAGTCCCCG CCACCCTGGC GGTGCTCCGC      180
AGGCACCGGG CCATCCGACA TCGCACCTCT GCTGGCGCGC ACGCTGGCCT GCTTGTGAAG      240
  
```

```

AGCATCCTTC AGCAGGCTGC CCAGCGGTGG CGCCTCCTGC ATAGACGCTT TGTTTTCAAA 300
AGTACTTGAC CTTTCCACAG CCTTCGGATA GACTTTCTTC TCTCTCTCTT CCAGCTTAAA 360
CAGAGCAAAG TTTTCCAAAT CACTCCCGGG TCCATGGGAT TTCTGGTGGG ATTCCTGTTT 420
CTCTGGGAAG CCGTCTGGTC GACGGCCTCT TTGGCCCTCG AGACA 465

```

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 694 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```

GNNNTCGTTG TTCCAGAACT TGATGAGGGG ATCTCGGAAC AACACNGAAA CTTTTCCCTC 60
CCTCANTNAC GCACCNCGAC TCTCTATTGA GCCAACGGNA ANNCGGCCCT TCCCTCCAAG 120
TAACTTTGNA TTTGAAAATA AAAAAAAAAA NTTGCTGTCC TTGCTATCCA AGAATAAATA 180
GACCTNCAAN TATTAATCTT TTGTTTCCCT CGTCATTGTT CTCGTTCCCT TTCTNCCTTG 240
TTTCTTTTTC TGCACAATAT ATCAAGCNAT ACCAAGCATA CAATCAAACCT CCAAGCTCGG 300
AATTCGGCCA NAGAGACCGT CGACGGAAGA AATTGNCTGG AAACCTGTTC ATGGTGATAT 360
ATACCGTCCN CCAAGAAAAG GGATGCTGCT ATCAGTCTTT CTAGGATCCG GGACACAGAT 420
ATTAATTATG ACCTTTGTGA CTCTATTTT CGCTTGCCTG GGAGTTTGT CACCTGCCAN 480
CCGAGGAGCG CTGATGACGT GTGCTGTGGT CCTGTGGGTG CTGCTGGGCA CCCCTGCAGG 540
CTATGTTGCT GCCAGATTCT ATAAGTCCTT TGGAGGTGAG AAGTGAAAAA CAAATGTTT 600
ATTAACATCA TTTCTTGTC CTGGGATTGT ATTTGCTGAC TTCTTTATAA TGAATCTGAT 660
CCTCTGGTCA ACGGCCTCTT TGGCCCTCGA GACA 694

```

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

AGACTCGTCT CAGACCAGTT GCAGCCTTCT CAACCCAAAC GCCGACCAAG GAAAACTCA 60
CTACCATGAG AATTGCAGTG ANTTGCTTTT GCCTCCTAGG CATCACCTGT GCATACCAG 120
NTAAACAGGC TGATTCTGGA AGTTCTGAGG AAAAGCAGCT TTACAACAAA TACCAGATG 180
CTGTGNCCAC ATGGCTAAAC CCTGACCCAT CTCAGAAACA GAATCTCCTA GCCCCACAGA 240
CCCTTCCAAG TAAGTCCANC GAAAGCCATG ACCACATGGA TGATATGGAT GATGAAGATG 300
ATGATGACCA TGTGGACAGC CAGGACTCCA TTGACTCGAG CGACTCTGAT GATGTAGATG 360
ACACTGATGA TTCTCACCAG TCTGATGAGC CTCACCATTC TGATGAATCT GATGAAGTGG 420
TCACTGATTT TCCCACGGAC CTGCCGTCGA CGGCCTCTT GGCCCTCGAG ACA 473

```

## (2) INFORMATION FOR SEQ ID NO:21:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```

AGAAGCTGTG ATCTTCAAGA CCATTGTGTC CAAGGAGATC TGTCTGATCC CAAGCAGAAG      60
TGGGTTCAGG ATTCCATGGA CCACCTGGAC AAGCAACCCA AAACCTCCGAA GACGTGAACA      120
CTCACTCCAC AACCCAAGAA TCTGCAGCTA ACTTATTTTC CCCTAGCTTT CCCCAGACGT      180
CGACGCCTCT TTGCCCTCGA GACA                                         204

```

## (2) INFORMATION FOR SEQ ID NO:22:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```

GTCCACACAC GCCGACCACG GAAAACACAC TACCATGAGA ATTGCAGTGA TTTGCTTTTG      60
CCTCCTAGGC ATCACCTGTG CCATACCACT TAAACAGGCT GATTCTGGAA GTTCTGAGGA      120
AAAGCAGCTT TACAACAAAT ACCCAGATGC TGTGGCCACA TGGCTAAACC CTGACCCATC      180
TCAGAAGCAG AATCTCCTAG CCCCACAGAA TGCTGTGTCC TCTGAAGAAA CCAATGACTT      240
TAAACAAGAG ACCCTTCCAA GTAAGTCCAA CGAAAGCCAT GACCACATGG ATGATATGGA      300
TGATGAAGAT GATGACGACC ATGTGGACAG CCAGGACTCC ATTGACTCGA ACGACTCTGA      360
TGATGTAGAT GACACTGATG ATTCTCACCA GTCTGATGAG TCTCACCATT CTGATGAATC      420
TGATGAACTG GTCACAGATT TTCCGTCGAC GGCTCTTTG GCCTCGAGA CA              472

```

## (2) INFORMATION FOR SEQ ID NO:23:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```

GTCGACTGAA AATTAACCCT CAGACGCCAC ATCCCCTGAC AAGATGCCAG GCAGGTTCTC      60
TTCCTCTCAC ATACTGACCC ACGGGTCCAC CCTCTCTCCC CTGGAAAGGA CACCATGAGC      120
ACTGAAAGCA TGATCCGCGA CGTGGAGCTG GCCGAGGAGG NNTTNNCCAA GAAGACAGGG      180
GGGGCCCAGG GGTCCAGGNG GNGCTTGTTT CTCAGACTCT TCTCCTTCCT GATCGTGCGA      240
GGNGNCACCA CGCTCTTCTG NCTGNTGNAC TTTGGAGTGG ATCCGGGCCC CAGAGGGAAG      300
AGTTCCCCCA GGGGACTCTT CTCTAATCNA GNCCTCTTGG                      340

```

## (2) INFORMATION FOR SEQ ID NO:24:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GTCGACGCGC GCCGGTAAAA ATGGCGAAAT GGGGGTAGGC GGCGCTGGAC CTGAAGAGAT	60
GGGGCGCGCA GGTGGGGCGG TTGTCAGAGC CCCCTGACGT GGGCGCCGGG CTTTATCGG	120
CGATTTGATC TGGCGACCTC GGGCCGCGC CTAAGAGGTC AGACTGCGGA GCCTGCGGGT	180
CGCCAGCGGC CCCGCCGAGT GCCGGAGGCA ATGGATGAAC AGAGCGTGGA GCGCTGKCTG	240
WCAGAGCAGA GAGCTCAATG TCCTCATTCC CGTGCTCCAC TCCAGCTACG AGAACTAGTA	300
AATTGTCGTT GGGCAGAAGA AGTAACACAA CAGCTTGATA CTCTCAACT CTGCAGTCTC	360
ACCAAACATG AAGAAAATGA AAAGGACAAA TGTGAAAATC ACCATGAAAA ACTTAGTGTA	420
TTTGTCTGGA CTTGTAAGAA GTGTATCTAC CATCAGTGTG CACTTTGGGT CGACGGCCTC	480
TTTGGCCCTC GAGACA	496

## (2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 267 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AGACACATAG ACCAACCGGG GAGATATGTT TGAATNTGAT GAAGATGAGA TGTTCTATGT	60
GGATCTGNAC AAGAAGGAGA CCTCTGTCTAT CTGGAGGAGA NTGNCCAACC CTTTCTCTT	120
GAGNCTCAGG GNGGGCTGTC TAACATTGCT ATANTGAACA ACAACNTGAA TACCTTGATC	180
CAGCGTTCCA ACCACACTCA GNCCACCAAC GATCCCCCTG AGGTGACCGT GTTCCCAAG	240
GTACGGCCT CTTTGGCCCT CGAGACA	267

## (2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 451 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GTCGACCTTG AAGATGTTTT CTAAAGAATC AAAAATGCTA CAAAGAAGTA TATCATTTTC	60
AAATATGGCT TTATCGTCTT GTTTACTTTT ACCAGGAGAT GCCACTGTCA TAACCTCTTC	120
ATGGGATAAT AATGTCTATT TTTATTCCAT AGCATTGGA AGACGCCAGG ACACGTAAAT	180
GGGACATGAT GATGCTGTTA GTAAGATCTG TTGGCATGAC AACAGGCTAT ATTCTGCATC	240
GTGGGACTCT ACAGTGAAGG TGTGGTCTGG TGTTCTGCA GAGATGCCAG GCACCAAAG	300
ACACCACTTT GACTTGCTGG CCGAGCTGGA ACATGATGTC AGTGTAGATA CAATCAGTTT	360
AAATGCTGCA AGCACACTGT TAGTTTCCGG CACCAAAGAA GGCACAGTGA ATATTGGGA	420
CCTCACAACG GCCTCTTTGG CCCTCGAGAC A	451

## (2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 456 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```

GTTGACGCAA GTTGCTGGGC TGGTGGGGGC CTGTCAAGTG AGGCCTGGTG GAGAAAGGTT      60
GAATTGGAG  GGCCAGGAAC AAGCTGGGAT GCAGGGGAGG CTTTCTAAAC TCTACAGTGC      120
TTCTAGAGAT GACGAGGAGG TAGGGAGTAG AAGAGAGCCG GACAGATTAG GGAGCTCCCA      180
GGGTGAGCTT GTGGGCAGSC CTSCAGAGGA GAAGAGGCTC TTCCCTAGGA GCTCAGAGGG      240
ACTTGTCTG  GAAGACTGAT GGGAGATGTA TGCAGCTGTT TAGAGGCTGC TTTGGAGAAC      300
AAATGAACAT GGTTCGTGTT GTGCAAGCAG TTACTGTGGT TCTTTTTCCT CATATATCTT      360
CCAATAAAGA CATTGAGCGA GGAGAGTTGA TACCGTCATG TTTTGGAGC  TTAAGCACAG      420
ACTGGCAGGT CGACGGCCTC TTTGGCCCTC GAGACA                                456

```

## (2) INFORMATION FOR SEQ ID NO:28:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```

GTCGACAGAA TTCACAACAT CCCAAGATTC CACCTCNCA  GATGTTTTCT AAAGNAATCA      60
AAAATGCTAC AAAGAAGTAT ATCATTTTCA AATATGGCTT TATCGTCTTG TTTACTTTTA      120
CCAGGAGATG CCACTGTTCAT AACTTCTTCA TGGGATAATA ATGCTATTTT TTATTCCATA      180
GCATTTGGAA GACGCCAGGA CACGTTAATG GGACATGATG ATGCTGTTAG TAAGGATCTG      240
TTGGCATGAC AACAGGCTAT ATTCTGCATC GTGGGACTCT ACAGTGAAGG TCGCGTCTGG      300
TGTTCCCTGC AGAGATGCCA GGCACCAAAA GACACCACTT TGGCTTGNTG GCCGAGCTGG      360
ACATGATGTC AGNGTNGGTA CAATCAAGNT TANNA                                395

```

## (2) INFORMATION FOR SEQ ID NO:29:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

```

GTGGNCCGAG ATAGAGGAGG CTTCCTCCA AGAGGACCCC GNGTTCCCG AGGGAACCCC      60
TCTNGAGGAG GAAACGTCCA GCACCGAGCT GGAGACTGGC AGTGTCCCAA TCCGGGTTGT      120
GGAAACCAGA ACTTCCCCTG GAGAACAGAG TGCAACCAGT GTAAGGCCCC AAAGMCTGAA      180
GGCTTCCTCC CGCCACCCTT TCCGCCCCCG GGTGGTGATC GTGRCAGAGR TGGCCCTGST      240
GGCATACGGG GAGGAAGAGR TGGCCTCATG GATCGTGGTG GTCCCGGTGG AATGTTTCTG      300
GRTGGYCGTK GTGGAGACAG AGRTGKCTTC CGTKGTGGCC GGGGCATGGA CCGAGGTGKC      360
TTTGGTGGAG GAAGACNAGG TGTCCCTGGG GGCCCCCTG NTCCTTTGAT GGAACAGATG      420
GGAGGAAGAA GAGGAGGACG TGGGTCGACG NCCTCTTTGT CCCTCGAGAC A                                471

```

## (2) INFORMATION FOR SEQ ID NO:30:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GTCGACCGTC	TACGCCTACA	CCATGTTCTT	CTCCACGTTT	TACCACGCCT	GCGACCAGCC	60
CGGGGAGGCG	GTGCTGTGCA	TCCTCAGCTA	CGACACGCTG	CAGTACTGCG	ACTTCTTGCG	120
ATCCGGGGCG	GCCATCTGGG	TCACCATCCT	GTGCATGGCA	CGGCTCAAGA	CAGTCCTGAA	180
ATACGTGCTG	TTTCTTCTGG	GTACACTGGT	CATCGCCATG	TCCTTGACAG	TGGACCGCAG	240
GGGCATGTGG	AACATGCTGG	GGCCCTGCCT	CTTTGCCTTC	GTGATCATGG	CCTCCATGTG	300
GGCTTACCGC	TGCGGGCACC	GGCGCCAGTG	CTACCCCACT	TCGTGGCAGC	GCTGGGCCTT	360
CTACCTCCTG	CCCGGCGTCT	CTACGGCCTC	TTTGGCCCTC	GAGACA		406

## (2) INFORMATION FOR SEQ ID NO:31:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GTCGCCCAGC	AAGTGAGCAG	ATCCTCCGAG	GCACCAGGGA	ACTCCAGCCC	ATGCCATGGC	60
GGATTCTGAG	CGCCTCTCGG	CTCCTGGCTG	CTGGGCGCGC	TGCACCAACT	TCTCGCGCAC	120
TCGAAAGGGA	ATCCTCCTGT	TTGNTGAGAT	TATATTATGC	CTGGTGATCC	TGATCTGCTT	180
CAGTGNCTCC	ACACCAGGCT	ACTCCTCCCT	GTCGGTGAYT	GAGATGATCC	YTSCTCSCTA	240
TCTTTCCTYT	GTTGTCTACA	TGTGTGACCT	GCACCACCAA	GATACCATTG	ATCAACTGSS	300
CCTGGAGTGA	TTTCTTCCGA	ACCCTCATAG	GGGSAATCCT	CTACCTGATC	AMCTCCATTG	360
TKGTCCTKGT	TGAGAGAGGA	AACCACCCCN	TNAATCGTTC	GTAGGGGTAC	TGGGCCTAAT	420
CGCTACGGCC	TCTTTGGCCC	TCGAGACA				448

## (2) INFORMATION FOR SEQ ID NO:32:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TTNCAATCNC	CGATCCCCAT	CACGAATGGG	GGGCACCGGG	TTACCCCCCC	CCTCCCGCCG	60
TAGGGTAGGC	ACACNCTGAG	CCAGTCAGTG	TATCGCGCGT	GCATCCCCGG	ACATCTAAGG	120
GCATCACAGA	CCTGTTNTTG	NTCAATCTCG	GGTGGNTGNN	CGCCACTTGT	CNCTCTAAGA	180
ANATGGGGGA	CGCCGNCCGC	TCGGGGGTNG	CGTAACTAGN	TAGNATNCCA	GAGTCTCGTT	240
CGTTATCGGA	AGTAACCAGA	CANATCGCTC	CNCCAATAA	GANNGGCCAT	NCACCACCAC	300
CCACGGAATC	GAGANAGAGC	TATCAATCTG	TTGTAGGACA	TAACCCGGCT	TCTTGGTTCAT	360
CATCNTGGTG	TACNCGNCCT	CTTGNCCCT	CGAGACA			397

## (2) INFORMATION FOR SEQ ID NO:33:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 365 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TCCTGCCTGC TGGGCCGCCT TNCACCCAAC TTCTCGCGCA CTCGAAAGGG AATCCTCCTG	60
TTTGCTGAGA TAAATANTAT NCCTGGTGAT CCTGATCTGC TTCAGTGCCT CCACACCAGA	120
CNACTCCTCC CTGTCGGTGA TTGAGATGAT CCTTGCTGCT ATTTTCTTTG TTGTCTACAT	180
GTGTGACCTG CACACCAAGA TACCATTCAT CAACTGGCCC TGGAGTGATT TCTTCCGAAC	240
CCTCATAGCG GCAATCCTCT ACCTGATCAC CNCCGTTGTT GTCCTTGTTG AGAGAGGAAA	300
CCACTCCTAC AATCGTCGCA GGGGTACTGG GCCTAATCGC TACGGCCTCT TTGGCCCTCG	360
AGACA	365

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GTCGACGACA CGCTGTCTTC ACTACCTGAT TGCCCAAG ATCCACACTG TCTACACTAC	60
CTGCCTGGCC AGTAGATCCA CGGTATCTAC ACTACCTCCC TGGCCAGCAG ATTCACCCAG	120
TCTACACTAA CCGCTTGTC AGCAGGTCCA CCCTGTCTAC ACTACGTGCC TGCCAGCAGA	180
TCCAAGCTGT CTACACTCCC TGCCTGGCCA GTAGATCCAT GCTATCTCCA CTACCTGCCT	240
ATCCAAGTGA TCCACCCTCT CTTTACTACC TTCCTGTCCG GCAGATTGAC CCTCTCTACT	300
CTACCTGCCT GGCCAGCAGA TCCACGCTAT CTACACTACC TGACTTACCA GATCCACCCCT	360
GTCTACACTA CATGCTTGTC CAGCAGGTCC ACCCTGTCTA CACTACCTGC CTCTCCAGAA	420
GATCCACGTC AACGGCCTCT TTGGCCCTCG AGACA	455

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGGANTTNGG CCCAAAGAGC CCGTTTGAGT NAACCNAAGA AGTCAAGATT GGCCCNAAGT	60
TCCAGANATG TTTTGAAGAC CTGGAGAACT GTTACAGTGN AAATGAAGAA GACAGTTCCT	120
CCATTGATCA TCTGTCTCTG AATCAGAAAT CCTTCTATCA TGTAAGCTAT GGCCCACTCC	180
ATGAAGGCTG CATGGATCAA TCTGTGTCTC TGAGNATCTC TGAAACCTCT AAAACATCCA	240
AGCTTACCTT CAAGGAGAGC ATGGTGGTAG TANCANCAA CGGGAAGGTT CTGAAGAAGA	300
GACGGTTGAG TTTAANCCAA TCCATCACTG ATGATGACCT GGAGGCCATC GCCAATGACT	360
CAGAGGAAGA AATCATCAAG CCTAGGTCAT CACCTTTTAG CTCCCCGAGC AATGTGAAAT	420
ACAACTTAT GAGGATCATC AAATACGAAT TCATCCTGAA TGACGCCCTC AATCAAAGGT	480
CGACGGCCTC TTTGGCCCTC GAGACA	506

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs

- (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CGGTAACGCN	GTTNTCCTNA	GGCGAGCTCA	GGGAGNACAA	GAAACCCTCC	CGTGGAGCAA	60
GAANGCCACA	AGCTCNCTTG	ATCTTGATTA	TCAGGACGAA	AACAGACCGT	GAAAGCGGGG	120
CCTCAGCATC	CTTCTGACCT	NNTGGGTNTT	AAGCAGGAGG	TGTCAGAAAA	GTTNCCACAG	180
GGATAACTGN	CTTGTGNCGN	CCAAGCGNTC	ATAGCGACGT	CGCTTTTGA	TCCTTCGATG	240
TCGGCTCTTC	CTATCATTGT	GAAGCAGAAT	TCACCAAGCG	TTGGATTGTT	CACCCACTAA	300
TAGGGAACGT	GAGCTGGGTT	TAGACCGTCG	TGAGACAGGT	TAGTTTTACC	CTACTGATGA	360
TGTGTTGTTG	CCATGGTAAT	CCTGCTCAGT	ACGAGAGGAA	CCGCAGGTTC	AGACATTGCG	420
TGTATGTGCT	TGGCTGAGGA	GCCAATGGTC	GACGGCCTCT	TTGGCCCTCG	AGACA	475

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GTGACCCGA	TGGAGGAGGA	GGAGGTTGAG	ACGTTGCGCT	TTCAGGCAGA	AATTGCCCAG	60
TTGATGTCAT	TGATNCATCA	ATACTTTCTA	CTCGANCAAA	GAGATCTTTC	TGAGAGAGCT	120
CATTTCAAAT	TCATCAGATG	CATTGGACNC	AATCCGGTAT	GAAAGCTTGA	CAGATCCCAG	180
TAAATTAGAC	TCTGGGAAAG	AGCTGCATAT	TAACCTTATA	CCGAACAAAN	AAGANCGAAC	240
TCTCACTATT	GTGGATACTG	GAATTGGAAT	GACCAAGGCT	GACTTGATCA	ATAACCTTGG	300
TACTATCGCC	AAGTCTGGAC	CAAAGCGTTC	ATGGAAGCTT	TGCAGGCTGG	TGCAGATATC	360
TCTATGATTG	GCCAGTTCGG	TGTTGGTTTT	TATTCTGCTT	ATTTGGGTGC	TGAGAAAGTA	420
ACTGTGATCA	CCGTCGACGG	CCTCTTTGGC	CNGCGAGACA			460

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TCAAGCAATA	CCCAAGCAAA	CAATCNACTC	CAANCTCGGA	ANTCGNCCNA	AGAGACCGTC	60
GACCCCGTGT	TCACNATGGT	AGNNACGCCG	NCTACCATCG	ANAGTTGATA	GGGCAGACGT	120
TCGNGTGGGT	CGTCTCCCCC	CCGGGGGGCG	TGCGATCGCC	CCGAGGTAT	CTAGAGTCAC	180
CACACCCGCC	GGCGCCCNCC	CCCCGNCCGN	NAAAAAAGA	GGGGCTGTCT	GGGNTGGTTT	240
TGNTNTGATA	AATANACGCA	TCCCCCCCCC	GNNGGGGNN	AGCGCCCGTC	GGCATGTATT	300
ANCTCTAGAA	TTACCACAGT	TATCCAAGTA	GGAGAGGAGC	GAGCGNCCAN	AGGANCCATA	360
NCTGATTAA	TGAGCCATTC	NCAGTTTCNC	TGTTCCGNCC	GTGCGTACGN	AACGACCTCT	420
TTGTNCNTAA	AGNCG					435



## (2) INFORMATION FOR SEQ ID NO:39:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

```

GTCGACCACA CTGCTGCTCA CGCTCAGCAA CCTCATGTTC CTGGCCCCCA TCGCCGTCTC      60
AGTGCGGCGA TTCTTCCTGG TGGAGGCCTC CGTCTACGCC TACACCATGT TCTTCTCCAC      120
GTTCTACCAC GCCTGCGACC AGCCCGGGGA GGCGGTGCTG TGCATCCTCA GCTACGACAC      180
GCTGCAGTAC TCGCACTTCT TGGGCTCCGG GGCGGCCATC TGGGTCACCA TCCTGTGCAT      240
GGCACGGCTC AAGACAGTCC TGAAATACGT GCTGTTCTT CTGGGTACAC TGGTCATCGC      300
CATGTCTTGG CAGCTGGACG GCAGGGGCAT GTGGAACCTG CTGGGGCCCT GCCTCTTTGC      360
CTTCGTGATG ATGGCCTCCA TGTGGGCTTA CCGCTGCGGG CACCGGCGCC AGTGCTACCC      420
CACCTCGTGG CAGCGCTGGG CCTTCTACCT CCGCCCGGC GTCTCTACGG CCTCTTTGGC      480
CCTCGAGACA                                     490

```

## (2) INFORMATION FOR SEQ ID NO:40:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

```

CGTCTCAGGC CAGTTNCANC CTTCTCANNC AGAACGGCGN CCCAAGGAAA ANCTCACTAC      60
CATGAAGAAT TGCAGTGATT TGCNTTTGCC TCCTAGGCAT CACCTGTGCC ATACCAGNTA      120
AANCAGGCTG ATTCTGGAAG TTNCTGAGGG AAAAAGCAGC TTTACAACAA ATACCCAGAT      180
GCTGTGGCCA CATGGCTAAA CCCTGANCCA TCTCAGAAGC AGAATCTCCT AGCCCCACAG      240
AATGCTGTGT CCTCTGAAGA AACCAATGAC TTAAACAAG AGACCCAAAC AAGTNAGTCC      300
NACGAAAGCC ATGACCACAT GGATGATATG GATGATGAAG ATGATGATGA CCATGTGGAC      360
AGCCAGGACT CCATTGACTC GNNCGACTCT GATGATGTAG ATGACACTGA TGATTCTCAC      420
CAGTCTGACG AGTCTACCA TTCTGATGAA TCTGATGAAC TGGTCACTGA TTTCCCACG      480
GACCTGCCGT CGACGGCCTC TTTGACCCTC GAGACA                                     516

```

## (2) INFORMATION FOR SEQ ID NO:41:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

```

GCCAAGACTC GTCTCAGNCC AGTTGCAGCC TTCTCANCCA AACNCCGACC CAAGGANAAC      60
TCCCCTACCA TGAGAATTGC AGTGATTTGC TTTTGCCTCC TAGGCATCAC CTGTGCCATA      120
CCAGTTAAAC AGGCTGATTC CTGGAAGTTC CTGAGGAAAA GCAGCTTTAC AACAAATACC      180

```

CAGATGCTGT GTCCACATGG CTAAACCCCTG ACCCATCTCA GAAGCAGAAT CTCCTAGCCC	240
CACAGAATGC TGTGTCTCT GAAGAAACCA ATGACTTTAA ACAAGAGANN CANCCAAGTA	300
AGTCCANCGA AAGCCATGAC CACATGGATG ATATGGATGA TGAAGATGAT GATGACCATG	360
TGGACAGCCA GGACTCCATT GACTCGANCG ACTCTGATGA TGATAGATGAC ACTGATGATT	420
CTCACCAGTC TGACGAGTCT CACCATTCTG ATGAATCTGA TGAAGTGGTC ACTGATTTTC	480
CCACGGACCT GCCGTCGACG GCCTCAATGN CCCTCGAGAC G	521

## (2) INFORMATION FOR SEQ ID NO:42:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GCAAGCAANC AATCCAACCC AAGNTNGGGA NTCGNCCNAA GAGNCCGTTG ANCAGAAGCC	60
ANTNATGGAT GANCAAGCGC ACCTTATCTC CAACAATGAG CAACTGNCCA TNCTGGGNCC	120
GGNCGCCCTG GGGCNCCGGA GAGCAAGTGC ANCCGCGGAG CCCTGTACAC AGGCTTTTCC	180
ATCCTGGTGA CTCTGCTCCT CGCTGGCCAG GCCACCACCG CCTACTTCCT GTACCAGCAG	240
CAGGNCCGGC TGGACAAACT GACAGTCACC TCCCAGAACC TGCAGCTGGA GAACCTGCGC	300
ATGAAGCTTC CCAAGCCTCC CAAGCCTGTG AGCAAGATGC GCATGNCCAC CCCGCTGCTG	360
ATGCAGGCGC TGCCCATGGG AGCCCTGCCC CAGGGGCCCA TGCAGAATGC CACCAAGTAT	420
GGCAACATGA CAGAGGACCA TGTGATGCAC CTGCTCCAGA ATGCTGACCC CCTGAAGGTG	480
TACCCGCCGT CGACGGCCTC TTTGGCCCTC GAGACA	516

## (2) INFORMATION FOR SEQ ID NO:43:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TGCTATCCNA GNATAAAATA AGACCCTGCA ANTATTAATC TTNTTTGTTT CCTCGTCATT	60
GTTCTCGTTC CCTNTCTTCG TTGTTTCTNN TTCTGCACAA TATNTTCAAG CTATACCGAG	120
CATACAATCA AACTCCAAGC TCGGAATTCG NCCAAAGAGG CCGTCGAGCC GAATTCTCCA	180
CNAGAATAGC ATTTCTGCTC ATCTGCATGG TCGCAGTCAC GAGCCAGATG NCCTGNTTIN	240
CCACAGTTGT AGCAGCATTG CTCTCGCTCT CTCTTGGGCT CTTTGCAGTC CTTGGCAATG	300
TGGCCGCCTC TACCGCAGTT ATAGCAGGCA TCCTCCTGAA GATCACAATC CTTGGCAAGA	360
TGACCAGACT CACCACAGCG ATAACAAATA TCTGGAAGAG ACGAGGAAAC AAAGTGGAAA	420
CCTCTATCCG AGGTAAACC ACCTCTGCCA CGGCTTCTCA TTCCACGACC ACGGCCTCTT	480
TGGCCCTCGA GACA	494

## (2) INFORMATION FOR SEQ ID NO:44:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CCTCCANATN	ANCTTTNTTC	CTCTCATTGT	NTCGTCCCTC	CTCCTTGTTT	TTTNTGCCCC	60
AAAATCCANC	AAANCCAACA	ACCATCCNCN	CCACCTGGAA	GTNGCCCAAA	GAGGCCGNAC	120
CAAGAAGTGT	CGATTCCTTT	GTNTGNAGGA	GCGACCAGGA	ACATCTACGG	TTGAGAAGAA	180
AGAAAGANTG	CCTTCGTCCA	TGTCTTCCTG	TGTGAANTTT	CCAGACATAG	CCCAGTCGAC	240
CAGCCTTCCC	CACNAGACTG	GAGCGTCTCT	ATTGTATNTG	GGTCCCTGTA	AGAGTAGAAG	300
GGTGAATAATC	CCANTGTGTC	TGAGTNTTGC	GCCNCCACCA	TAAACACCGC	CTTTTCTCTG	360
AATTTCTGTA	TNCAAGAAAN	TGTCAGTCAT	CACACGTGCA	AGGATNTTAA	GACTGNCATG	420
ATCTGGGNCC	GTGTAGGGGN	CAGNTCGGAT	NCATTACCCC	ACGTAATTCA	CCGGGANGGG	480
CATCAGGAAG	TGAGTCTTCA	TCTCCAGGG	CGTGNAGGTG	GGTNCCATGA	CCAGCTTCCT	540
AATGACCTGG	GAGCCATGGG	GAACGTGGGC	ATCTCCACCA	GAGCTACTGG	GCACAGGTTT	600
CTCGACCGTG	TGTGGNCGCA	CAGACCGTCG	ACGGCCTCTT	TGNCCCTCGA	GACA	654

## (2) INFORMATION FOR SEQ ID NO:45:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GTGACCTGA	GAATCTGGAA	AAATTGGAGA	AGTTGGGTAT	GAGCTCAGAC	CTGGTGAGCA	60
GGTGCCTAC	CATTTATAGA	AATGCACATG	ACATCAAGAA	TAAGAGCTCT	GCCCCCAGCA	120
GAGTGCCTCC	TCTTTTGTG	CCACAGGGGA	CTTCTGAAAG	AAAAGACAGT	TCAGGTTCTG	180
TGTCCCCAMA	CACCTCTAGC	CAGGAGGAGG	GTGATCAGAT	CTGTTTGTKC	CATATCCGGA	240
AAAGTTGTAG	CTTTCAAGAT	AAGTGCCATA	GAGTTCATTT	CCATTGCGCG	YATCGATGGC	300
AATTCTTGGA	TAGAGGCAAA	TGGGAGGATT	TGGACNACAT	GGAACNTATT	GTAGAGNCAT	360
ATTGCAATCC	CCCCATAGAA	AGGATCCTGT	GCTCTGAGTC	AGCCAGTACC	TTTCACTCTC	420
ATTGTCTGAA	CTNTAACGCC	ATGACTTACG	GTGCTACCCA	GGCTCGCCGC	CTCTCCACGG	480
CCTCTTTGGC	CCTCGAGACA					500

## (2) INFORMATION FOR SEQ ID NO:46:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GTGACACAA	ATGTTTCCTT	GGATAATCCA	GCTTTACATG	GTGAGAACCA	TGCTAGAGTC	60
CCTCATTGCA	GACAAAAGTG	GTCCAAGAA	AACCTTGAGA	AGTAGCCTTG	AGGGGCCCCAC	120
CATATTGGAC	ATAGAAAAAT	TTCATCGAGA	GTCATTCTTC	TACACTCACT	TGATAAATTT	180
CAGTGAAACG	CTGCAGCAGT	GCTGTGACCT	TTCGCAGCTG	TGTTTCCGAG	AGTTCTTCCT	240
GGAGCTGACC	ATGGGCAGGA	GGATCCAGTT	CCCCATTGAG	ATGTCGATGC	CCTGGATCCT	300
GACGGACCAC	ATCCTGGAGA	CCAAGGAGGC	ATCGATGATG	GAGTACGTGC	TCTACTCCCT	360
GGACCTGTAC	AATGACAGCG	CCCCTACGC	GCTCACCAGG	TTCAACAAGC	AGTTCTCTTA	420
CGACGAAATT	GAGGCCGAGG	TCACGGCCTC	TTGGCCCTC	GAGACA		466

## (2) INFORMATION FOR SEQ ID NO:47:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

```

GTCGACGGAA GTTGATTTTT AATGATAAAG TACAATGAAG GGAGGGCAGA GGGGCTAAGC      60
CTAGCTGTCT GGGGTGCTGT GGTGGTGGTA GACTGGCTAC ACAAAGTGTG GCTGCTGCTG      120
CTGCTTCTTG GTGGCCGCCT TGCTGGCGAG GTCTTGGCC TTCTCTGTAG CTGCCAGTGC      180
CGTCTCCTTT GCCTTCTCCT TGGCTTCCTT GGCTGTCTCA ACAAGTGTGTT TGAAGGGGC      240
CTCGCCTTGC AGCTTAGCCA AGATATATTC AAAACCCCTC ATAGTCTTGG TCACGTTGCT      300
TTTGAACCGG GCAAGACCAA ATCCTGGAC AGCTCTGGCT ACACAACTG TTGCTGGTCA      360
ACGGCCTCTT TGGCCCTCGA GACA

```

## (2) INFORMATION FOR SEQ ID NO:48:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

```

GTGACGGGAC AAAAATCTAG GGAGGCACCA ATCCTGAAAG AGTTTAAGGA AGAAGGGGAA      60
GAGATACCTA GAGTAAAACC AGAGGAGATG ATGGATGAGA GACCCAAAAC AAGATCCCAG      120
GAACAGGAGG TGTTAGAGAG AGGAGGGAGA TTTACAAGAT CCCAGGAAGA GGCTAGAAAA      180
AGTCATCTGG CCAGACAGCA GCAGGAGAAG GAAATGAAAA CAACATCTCC CCTTGAGGAG      240
GAAGAAAGAG AAATAAAATC TTCACAAGGC TTAAAGGAAA AATCGAAGTC TCCTTCCCCT      300
CCTCGACTGA CTGAAGATCG AAAGAAGGCC CCACTTGTAG CGCTGCCAGA GCAAAGTGCC      360
AGCGAGGAGG AGACTCCTCC ACCTTTACTA ACAAAGGAAG CATCTTCTCC ACCACCTCAT      420
CCACAGCTCC ATAGCGAAGA AGAAATAGAG CCCATGGAAG GCCCAGCCCC CCCTGTCCTC      480
ATTCAGTTAT CTCCTCCTAA TACAGATGCT GACACCAGGT CGACGGCCTC TTTGGCCCTC      540
GAGACA

```

## (2) INFORMATION FOR SEQ ID NO:49:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 520 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

```

GTCGACGTCG GTGGTGCGAG CGGCGGCGGC GGCGTTCCA GCATGAAGAG GAGAGCTGGC      60
CTGGGGGGCA GCATGAGGTC AGTGGTGGGC TTCTGTCCC AGCGGGGCTC GCATGGGGAC      120
CCCTGTCTCA CTCAGACTT TCAGAGGAGA CRCCTGCGGG GCTGCAGAAA CCTCTACAAG      180
AAGGACCTCC TCGGCCACTT CGGCTGTGTC AATGCCATTG AATTCTCAA CAATGGAGGC      240
CAGTGGCTGG TCTCAGGAGG AGATGACCGC CGGGTCTGTC TATGGCACAT GGAACAAGCC      300
ATCCACTCCA GGGTCAAGCC CATACAGCTG AAAGGAGAGC ACCATTCAA CATTTTTTGC      360

```

CTGGCTTTCA ACAGTGGGTA CACTAAAGTG TTCTCTGGAG GCAATGATGA GCAAGTTATC	420
CTCCATGATG TTGNAAGCAG TGAGACATTG GACGTGTTTG CTCATGAAGA TGCAGTATAT	480
GACTTGCTCTG TGGTCNGCGC CCTCTTTGGC CCTCGAGACA	520

## (2) INFORMATION FOR SEQ ID NO:50:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GTGCGACTCCA GACACACCCC CCAGTCGAGC CCTGCAGCCA AACAGAGCCT TCACAACCAG	60
CCACACAGAG CCTGCCTCAG CTGCTCGCAC AGATTACTTC AGGGCTGGAA AAGTCACACA	120
GACACACAAA ATGTCACAAAT CCTGTCCCTC ACTCAACACA AACCCCAAAG CACAGAGAGC	180
CTGCCTCAGT ACACTCAAAC AACCTCAAAG CTGCATCATC ACACAATCAC ACACAAGCAC	240
AGCCCTGACA ACCCACACAC CCCAAGGCAC GCACCCACAG CCAGCCTCAG GGCCACAGG	300
GGCACTGTCA ACACAGGGGT GTGCCAGAG GCCTACACAG AAGCAGCGTC AGTACCCTCA	360
GGATCTGAGG TCCCAACACG TGCTCGCTCA CACACACGGC CTGTTAGAAT TCACCTGTGT	420
ATCTCACGCA TATGCACACG CACAGCCCTC AACGGCCTCT TTGGCCCTCG AGACA	475

## (2) INFORMATION FOR SEQ ID NO:51:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CCTGCCACAA TAATNTCCNA AGCCTAAAAC CCGAGCAATA CAANCNAACC CAAGCTCGGA	60
AATCGGGCCA AAGAGACCGT TCTTAGNTGG TGGAGCGATT TGTCTGGTTN ATTCCGATAA	120
ACGAACGAGA CTCTGGCATG CTAAGTAGTT ACGCGACCCC CGAGCGGTCTG GCGTCCCCCA	180
ACTTCTTAGA GGGACAAGTG NCGTTCANCC CACCCGAGAT TGAGCAATAA CAGGTCTGTG	240
ATGCCCTTAG ATGTCCGGGG CTGCACGCGC GCTACACTGA CTGGCTCAGC GTGTGCCTAC	300
CCTACGCCGG CAGGCGCGGG TAACCCGTTG AACCCCATTC GTGATGGGGA TCGGGGATTG	360
CAATTATTCC CCATGAACGA GGAATTCCCA GTAAGTGCGG GTCATAAGCT TGCATTGATT	420
AAGTCCCTGT CGACGGCCTC TTTGGCCCTC GAGACA	456

## (2) INFORMATION FOR SEQ ID NO:52:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GTGCGRRCAA SMTYTYTMMA CTGTGGNGGG GCTCTACCCN TGAGGGCCTG GCCGCARCNT	60
---	----

GGCTGSGGGC	TGWCGACTAT	GAACAGRTCG	AGAAMGTGKN	CGATTACTAC	CCGGAGTACA	120
AGCTRCTCTY	CGAGGGTGCA	GGTAGGCAAC	CCTGGAGACA	TGACKCTGGA	GGGMCGATTA	180
CTTTGAGYAC	GAGGTAAARC	TGAACAAGTT	GTSCCTCCTG	ANACAGTWCC	ACCTTGGTGT	240
CTTCTATRCC	TTCGTGAAGC	TCAAGGAGCA	GGAGTGTCKC	AACATCGTGT	GGATCGCTGA	300
ATGTATCTRC	CAACGCMSS	GCRMMYCSMA	MSWCAWCCWY	ATTCTSTRTC	CTKSYAASGT	360
CWCAMTGAAN	CWAGCCCTCT	CAATTGCACT	GCACTGTGTG	TGTGTGTGTG	TGTGTTGTGC	420
GTGTGTGTTG	CGTGTGTGTG	TATGTGGTCT	GTGACAAGCC	TGTGGCTCAC	CTGGTCGACG	480
GCCTCTTTGG	CCCTCGAGAC	A				501

## (2) INFORMATION FOR SEQ ID NO:53:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CCNCCGTTTG	TTGTNNTGCA	CCAAANANCC	NCNAATTGNC	CANANAAAAT	TGATGGGAAG	60
ACCACTTAAA	GGGGGGGNAN	TTAGGCGGGN	CAAAGACAAG	GCACCCNACA	AGATGTCGTT	120
TGTTCCAGAG	CTGATTGAGG	GGTATCTCGG	AAGNAACACN	GAAACTTTTT	TCCTTCCTTC	180
AATTCAACGC	ACACTACTCT	CTAATGAGCN	NCGGAATACG	GCCTTCCTTC	CAGTTACTTG	240
AATNTGAAAT	AAAAAAAAGT	TTGCTGTCTT	GCTATCCAAG	TATAAATAGA	CCTGCAATTA	300
TTAATCTTTT	GTTTCCTCGT	CATTGTTCTC	GTTCCCTTTC	TTCCTTGTTT	CTTTTCTGTC	360
ACAATATTTT	AAGCTATACC	AAGCATACAA	TCAACTCCAA	GCTCGGAATT	CGGCCAAAGA	420
GGCCGTCGAC	GAACCACCGG	CTGAAAATTG	GCTTCTTCAA	CCAGCAGTAT	GCAGAGCAGC	480
TGCGCATGGA	GGAGACGCCC	ACTGAGTACC	TGCAGCGGGG	CTTCAACCTG	CCCTACCAGG	540
ATGCCCGCAA	GTGCTTGGGC	CGCTTTGGCC	CTCGAGACA			579

## (2) INFORMATION FOR SEQ ID NO:54:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CCTGCNCCAA	NANTTCCNAA	CCNAATAACC	CAANAANACC	AATCCNNNCT	CCANCTGGGG	60
AATTCCGNCC	NAAGAGACCG	TTGTNTTGAT	GACAAGTCGA	AGCCAANAAT	ACCATNCAAC	120
CTGCTCCCAA	TCATGCAGGN	TNCNGCCACT	GCTGCCCTTG	CCGTCCCTCC	TCTGCACCAT	180
GGCTNCTCCT	GCAACCAGGT	CCTCTCTGCA	CCAATTGCTG	CTGANACGCC	GACCGCTGTC	240
TGCTTCAGCT	ACACCTCCCG	ACAGATTCCA	CAGAATTTC	TAGCTGACTA	CTTTGAGACG	300
AGCAGCCAGT	ACTCCAAGCC	CAGTGTCTATC	TTCCTAACCA	AGAGAGGCCG	GCAGGTCTGT	360
NNTGACCCCA	GTGAGGAGTG	GGTCCAGAAA	TACGTCAGTG	ACCTGGAGCT	GAGTGCCAGA	420
GGGGTCCAGA	AGCTTCGAGG	CCCAGCGACC	TCAGTGGGCC	CAGTGGGGAG	GAGCAGGAGC	480
CTGANCTTGG	GGAACATGCG	TGTGACCTCT	ACAGCTACCT	CGTCGACGGC	CTCTTTGGCC	540
CTCGAGACA						549

## (2) INFORMATION FOR SEQ ID NO:55:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

```

GTCGACCTCC CAGGTCATTA GGAAGCTGGT CATGGAACCC ACCTTCAAGC CCTGGCAGAT   60
GAAGACTCAC TTCCTGATGC CCTTCCCGGT GAATTACGTG GGTGAATGCA TCCGAAGTGT   120
CCCCTACACG GACCCAGATC ATGCCAGTCT TAAATCCTT GCACGTTTGA TGAAGTCCAA   180
ATTCTTGCAT ACAGAAATTG GTGAAAAAGG CGGTGCTTAT GGTGGAGGCG CAAAAGTCTAG   240
CCACAATGGG ATTTTCACCC TTTACTCTTA CAGGGACCCA AATACAATAG AGACGCTCCA   300
GTCTTTTGGG AAGGCTGTCG ACTGGGCTAA GTCTGGAAAA TTCACACAGC AAGACATCGA   360
CGAAGCCAAA CTTTCTGTCT TCTCAACCGT AGATGCTCCT GTCGCTCCTT CAGACAAAGG   420
AATGGACCAC TTCTGTACG GCCTCTTTGG CCCTCGAGAC A                      461

```

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 511 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

```

GTCGACAATA ATTCCACCTC ACCAGGATAA TACCCATCCT TCAGCACCAA TGCTCCACC   60
TTCTGTTGTG ATACTGAATT CAACTCTAAT ACACAGCAAC AGAAAATCAA AACCTGAGTG   120
GTCACGTGAT AGTCATAACC CTAGCACTGT ACTGGCAAGC CAGGCCAGTG GTCAGCCAAA   180
CAAGATGCAG ACTTTGACAC AGGACCAGTC TCAAGCCAAA CTGGAAGACT TCTTTGTCTA   240
CCCAGCTGAA CAGCCCCAGA TTGGAGAAGT TGAAGAGTCA AATCCATCTG CAAAGGAAGA   300
CAGTAACCTT AATTCTAGTG GAGAAGATGC TTTCAAAGAA ATCTTTCAAT CCAATTCACC   360
GGAAGAATCT GAATTCGCGG TGCAAGCGCC TGGGTCTCCC CTAGTGGCTT CCTCTTTATT   420
AGCTCCTAGC AGTGGCCTTT CAGTTCAAAC TTCCCACCAG GGCTTTACTG CAAAACAAGC   480
ACGGTCAACG GCCTCTTTGG CCCTCGAGAC A                      511

```

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 483 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

```

GTCGACAGTC CAAAGTCTCA AGACAGTTAT CCTGTTAGTC CTCGACCTTT TAGTAGTCCA   60
AGTATGAGCC CCAGCCATGG AATGAATATC CACAATTTAG CATCAGGCAA AGGAAGCACC   120
GCACATTTTT CAGGTTTTGA AAGTTGTAGT AATGGTGTAA TATCAAATAA AGCACATCAA   180
TCATATTGCC ATAGTAATAA ACACCACTCA TCCAAGTTGA ATGTACCAGA ACTAAACAGT   240
ATAAATATGT CAAGATCACA GCAAGTTAAT AACTTCACCA GTAATGATGT AGACATGGAA   300
ACAGATCACT ACTCCAATGG AGTTGSAGAA ACTTCATCCA ATGGTTTCCT AAATGGTAGC   360
TCTAAACATG ACCACGAAAT GGAAGATTGT GACACCGAAA TGGAAGTTGA TTCAAGTCAG   420
TTGAGACGCC AGTTGTGTGG AGGAAGTCAG GCCGCGTCTA CGGCCTCTTT GGCCCTCGAG   480
ACA                      483

```

## (2) INFORMATION FOR SEQ ID NO:58:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

```

GTCGACGAGG TGGTGATCAT GGAAGACGCC CCTGACTATT ATGCAGTGGA AGACATTTTC      60
AGCGAGATCT CAGACATTGA TGAGACAATT CATGACATCA AGATCTCTGA CTTCATGGAG      120
ACCACCGACT ACTTCGAGAC CACTGACAAT GAGATAACTG ACATCAATGA GAACATCTGC      180
GACAGCGAGA ATCCTGACCA CAATGAGGTC CCCAACAACG AGACCACTGA TAACAACGAG      240
AGTGCTGATG ACCACGAAAC CACTGACAAC AATGAGAGTG CAGATGACAA CAACGAGAAT      300
CCTGAAGACA ATAACAAGAA CACTGATGAC AACGAAGAGA ACCCTAACAA CAACGAGAAC      360
ACTTACGGCA ACAACTTCTT CAAAGGTGGC TTCTGGGGCA GCCATGGCAA CAACCAGGAC      420
AGCAGCGACA GTGACAATGA AGCAGATGAG GCCAGTGATG ATGAAGATAA TGATGGCAAC      480
GAAGGTGACA ATGAGGTCAC GGCCTCTTTG GCCCTCGAGA CA                          522

```

## (2) INFORMATION FOR SEQ ID NO:59:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

```

GTCGACAGAT CATGTTGGAA GAGCCCCCAG TAGCAAAAGT GTTAGAGCCT TCAGAAACCC      60
TTGTGGTATC ATCAGAGACA CCTACTGAGG TGTACCCTGA GCCAAGCACA TCAACAACAA      120
TGGATTTTCC AGAGTCATCT GCAATTGAAG CGCTAAGATT GCCAGAGCAG CCTGTAGACG      180
TACCATCGGA GATTGCAGAT TCATCCATGA CAAGACCGCA GGAGTTGCCG GAGCTGCCTA      240
AGACCACAGC GTTGGAGCTG CAGGAGTCGT CGGTGGCCTC AGCGATGGAG TTGCCGGGGC      300
CACCTGCGAC CTCCATGCCG GAGTTGCAGG GGCCCCCTGT GACTCCAGTG CTGGAGTTAC      360
CTGGGCCCTC TGCTACCCCG GTGCCAGAGT TGCCAGGGCC CCTTTCTACC CCAGTGCCTG      420
AGTTGCCAGG GCCCCCTGCG ACAGCAGTGC CTGAGTTGCC AGGGCCCTCT GTGACACCAG      480
TGCCACAGTT GTCGAGGAA TTGCCGTCAA CGGCCTCTTT GGCCCTCGAG ACA                          533

```

## (2) INFORMATION FOR SEQ ID NO:60:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

```

CCACCAGACA TAAAGTACTG ACATGATCAG AGGAATCATC AGCAACTGCA TNTCCATTGC      60
TAAGCCAGTA ATCACGATGC AAATCCAGTT AAAGAGGAGC ATGAATAAAT AGTCTGCTGG      120
CCTCCCATCA AAAGCTCCTG TTTCAAGTCG CGTAGAATAC TGATATAAGA AATATANATT      180

```



GACCAAATAA	AGAAATCCAG	TTCCTGGACC	CACAGGGAAA	TAAAAGGTGG	CAGTGATTGN	240
CCTCCAAATC	TGAAAGCGAT	ANAGGAAGGC	TTCGGGCCAG	AGGAAGAGGT	AGGCCGGGCT	300
GATGAGGCCG	AGTTTGCCGA	CCAAGGGCAC	GGNGACGGTG	GCGGCGAACC	AATAGCGCGT	360
GATCGCCGGG	ATGCTCCTGA	ACCAGTCTCC	GATGTCCGAC	ATCTTCGACC	CACAGGTAGC	420
CAAGATGCAC	AAGACCGCCC	GACTCCCCGC	GCCGACCCCC	TCACGACGCG	GCCGGCTCCG	480
CGACTGTTAG	GTGTCTAGGT	GGAAGCCGCG	TCGAC			515

## (2) INFORMATION FOR SEQ ID NO:61:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

ATNCNGGAGN	CCCAGATGCT	GTGGGCCCATG	ATCGCANNTT	GNNTGAGAGA	ATTGGCAGAA	60
NCAGANTACT	CCTAGCNAGA	NCAGTATTNT	GTGTNACTCT	GGAGAATTNC	AGTGATGNAA	120
AAAAANAGAC	CNGTNCAAGT	AAGTCCAGCG	AAAAGCATGC	CCACATGGAT	GAANTGGATG	180
ATGAAGATGA	TGCCNNCCNT	GNGGNCAGCA	GGAACCTCTN	TNNCTGCGNG	NCNACTCNTG	240
NTGNTGTAGA	TGANGCTGGT	NAAGCNNANC	AGTCTGNTGA	GNCTCCTCGA	GTCTGATGGA	300
TCTNATGAGC	AGANCGNTGA	TTCGTGNGCC	GCCGTNCTCC	TTNGAGCCCN	CNAGACA	357

## (2) INFORMATION FOR SEQ ID NO:62:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CTTGATAGATG	GAGCGGGGAG	NCAGACTNCT	GGNGCTGCG	TGANTGCTGA	CGTGAGATGG	60
ATTAATTAAT	GGCNAGCAAG	NATGGNGNCT	NCGAGCCCCCT	CCCTGNNCGT	NCCTNCCAGN	120
NGTGGCAATN	GCGTACGTGG	NCAGACTTCA	GGNAGAAAAA	AAAAAAANGG	GNCNCGTAAG	180
CTGCTGCGGG	NNCAGCAGCT	TGAGACTGNC	AAGTGACTCA	GATGCAGAGT	CAGACTNTCG	240
GGCTAGCTCT	AACAACTCCN	CCGTCTCCAA	CACCAGCACC	GAGGGCTTCG	GGGACATCAT	300
GTCTTTGACC	AGCAGCCTCT	ATCGGAACCA	CAGTACCAGC	TTCACTCTTT	CAAACCTCAC	360
ACTNCCGTG	NCGGCCTCNT	TGGCCTTTNG	AGGCGA			396

## (2) INFORMATION FOR SEQ ID NO:63:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GTCGACCCCA	GATGAAATGT	CATGGCAAAT	TTGATAAAAA	CCAAGAGGGA	GTGAAACTGA	60
------------	------------	------------	------------	------------	------------	----

CGCTGGGGGA	GGGAAGGGTC	AAGTCGAGGG	AAGGTGAAAC	CAAAAGGCAC	TGAGCATGCG	120
TGGTGGGGCA	GGGAAGGACA	CCATCACTCC	AGAGACAGTA	TGGTAACAAA	GGGACAGGAA	180
TGGTCCAGGC	CAGCTTCAGG	CTCTTCAGAA	GCCAGAGAGA	TGTCCAAGTC	TACCAAACCG	240
AGTTCTCCAA	GGCTTTTCAA	GAAATGGGAT	TTGCTTGCAA	GATGAATGAG	GGAGGAGGTC	300
CCATGGCTTC	TAAGAGATCA	ACCCAAGTCT	TCCAATACTC	ACTGCTAAGT	CCCACCTGGG	360
TCCCCCAGAG	CCAGGAAGCT	CCCTGGTGGC	AGGTCCCCCT	CTTGCCCTCA	CGGCCTCTTT	420
GGCCCTCGAG	ACA					433

## (2) INFORMATION FOR SEQ ID NO:64:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GTCCACAAAA	TAGTTCTGTT	AAAGAATACC	GAATGGAAGT	TCCATCTTCG	TTTTCAGAAG	60
ACATGTCAAA	TATCAGGTCA	CAGCATGCAG	AAGAACAGTC	CAACAATGGT	AGATATGACG	120
ATTGTAAAGA	ATTTAAAGAC	CTCCACTGTT	CCAAGGATTC	TACCCTAGCT	GAGGAAGAAT	180
CTGGGTTCCC	TTCTACTTCT	ATCTCTGCAG	TTCTGTCTGA	CTTAGCTGAC	TTGAGAAGCT	240
GTGATGGCCA	AGCTTTGCC	TCCCAGGACC	CTGAGGTTGC	TTTATCTCTC	AGTTGTGGCC	300
GTTCCAGAGG	ACTCTTTAGT	CATATGCAGC	AACATGACAT	TTTAGATAACC	CTGTGTAGGA	360
CCATTGAATC	TACAATCCAT	GTCTGCACAA	GGATATCTGG	CAAAGGAAAC	CAAGCTGCTT	420
CTTGGTCAAC	GGCCTCTTTG	GCCCTCGAGA	CA			452

## (2) INFORMATION FOR SEQ ID NO:65:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

CTNAAANTTA	CCATCACAGT	TNCTACAATC	GGCTCTTCC	AATTTGGCNA	CAACNCTGGG	60
TCATCAATGC	TCCTGAGAAG	ATCATAAAGG	AATTTATCAA	TAAAACTTTG	TCGGACAAGG	120
GAAATNCCCC	ACCCTCTGAG	GTGCTGCTCA	CGTCTCTCTG	GTCCTTGCTT	GTGACCATAT	180
TTTCCGTCGG	GGGNATGATC	GGCTCCTTTT	CCGTCGGACT	CTTCGTCAAC	CGCTTTGGCA	240
GGCGCAANNC	AATGCTGATT	GTCAACCTGT	TGGCTGTCAC	TGGTGGCTGC	TTTATGGGAC	300
TGTGTAAAGT	AGCTAAGTCG	GTTGAAATGC	TGATCCTGGG	TCGCTTGGTT	ATTGGCCTCT	360
TCTGCCGACT	CTGGTCGACG	GCCTCTTTGG	CCCTCGAGAC	A		401

## (2) INFORMATION FOR SEQ ID NO:66:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GTTGAGAGCA	GCATGTTTTN	NCCACTGAAA	CTCATCCTGC	TGCCAGTGTT	ACTGGATTAT	60
TCCTTGGGCC	TGAATGACTT	GAATGTTTCC	CCGCCTGAGC	TAACAGTCCA	TGTGGGTGAT	120
TCAACTCTGA	TGGGATGTGT	TTCCAGAGC	ACAGAAGACA	AATGTATATT	CAAGATAGAC	180
TGGACTCTGT	CACCAGGAGA	GCACGCCAAG	GACGAATATG	TGCTATACTA	TTACTCCAAT	240
CTCAGTGTGC	CTATTGGGCG	CTTCCAGAAC	CGCGTACACT	TGATGGGGGA	CATCTTATGC	300
AATGATGGCT	CTCTCCTGCT	CCAAGATGTG	CAAGAGGCTG	ACCAGGGAAC	CTATATCTGT	360
GAAATCCGCC	TCAAAGGGGA	GAGCCAGGTG	TTCAAGAAGG	CGGTGGTACC	GCATGTGCTT	420
CCAGAGGAGC	CCAAAGAGCT	CATGGTCCAT	GTGGGTGGAT	TGATTCAGAT	GGGATGTGTT	480
TTCCAGAGCA	CAGAAGTGAA	ACACGTGACC	AAGGTAGAAT	GGATATTTTC	GTCGACGGCC	540
TCTTTGGCCC	TCGAGACA					558

## (2) INFORMATION FOR SEQ ID NO:67:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 539 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GTGGAGAAAA	TTGCTGCTGA	GAAGGACATT	TTGAAGGTTT	TGTTGGCTGA	AAAAGCTGTT	60
TCTGGAATCA	CCCTAGATC	TTTCTTGAAG	ACTTGAATTA	GATTACAGCG	ATGGGGACAC	120
AGAAGGTCAC	CCCAGCTCTG	ATATTTGCCA	TCACAGTTGC	TACAATCGGC	TCTTTCCAAT	180
TTGGCTACAA	CACTGGGGTC	ATCAATGCTC	CTGAGAAGAT	CATAAAGGAA	TTTATCAATA	240
AAACTTTGAC	GGACAAGGGA	AATGCCCCAC	CCTCTGAGGT	GCTGCTCACG	TCTCTCTGGT	300
CCTTGTCTGT	GGCCATATTT	TCCGTGCGGG	GTATGATCGG	CTCCTTTTCC	GTCGGACTCT	360
TCGTCAACCG	CTTTGGCAGG	CGCAANTCAA	TGCTGATTGT	CAACCTGTTG	GCTGTCACTG	420
TGACTGCTT	TATGGGACTG	TGTAAAGTAG	CTAAGTCGGT	TGAAATGCTG	ATCCTGGGTC	480
GCTTGGTTAT	TGGCCTCTTC	TGCGGACTCT	GGTCGACGGC	CTCTTTGGCC	CTCGAGACA	539

## (2) INFORMATION FOR SEQ ID NO:68:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 365 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GTTGACCCCA	TTTCCACCA	CCAAGCAAGC	AGAGCCTGTT	GTTTTGTCCA	AAATCAAAAC	60
TGCACATCCA	CAGAGCAGAG	ATCTCAAAGA	TTATGCGAGA	ATGTCAGGAA	GAAAGTTTCT	120
GGAAGAGAGC	TCTGCCTTTT	TCTCTTGTA	GCATGCTTGT	CACCCAGGGA	CTAGTCTACC	180
AAGGTTATTT	GGCAGCTAAT	TCTAGATTG	GACCATTGCC	CAAAGTTGCA	CTTGCTGGTC	240
TCTTGGGATT	TGGCCTTGGA	AAGGTATCAT	ACATAGGAGT	ATGCCAGAGT	AAATTCCATT	300
TTTTTGAAGA	TCAGCTCCGT	GGGGCTGGTT	TTGGTCCGTC	GACGGCCTCT	TTGGCCCTCG	360
AGACA						365

## (2) INFORMATION FOR SEQ ID NO:69:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GTCGACCTCG	GTAAATGCCT	CAGTTCCCCT	CCCAGATGGA	GGCATCGTTG	TGAGAGTCTG	60
ATTGGGAGGG	GAATATGAAA	ATGTTTTCGG	AAGATAAAAG	TACTACACAG	ATGTGAGGTG	120
GTTTTGCCTT	GGAAGAAAGT	GTCCTTAGA	TGTGTCTGGA	TGTTATGCAG	AGTGATCGTG	180
GCGTGTCAAT	CTTTCTTTTG	GGTGTTTTGC	AGCCTGAGAC	ATAAGGTAAT	TGTCAGAAAA	240
GGGAGACGTA	GAAGTGTGGA	TCTGTGGAAG	CTCACTCTTA	ACAAGAATTC	TAAGATGCAC	300
ATTTAAGTAC	TTGCCATGAC	GTGAGGTGTT	GTCACACGTC	AACCCTGAGA	TGCTGTCAGT	360
GTCACAGGGG	ACTTGACATT	TATGTTACCC	AGGAATGACT	GTGTAAATGT	GCAGGTGCAG	420
GCCGGGCGCC	GTGGCTCAGT	GCCTGTAATC	CCAGCACTTT	GGGAGCCCCG	TCGACGGCCT	480
CTTTGGCCCT	CGAGACA					497

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GTAGACANCA	NTAGAAAAAC	AAAAATCTCA	TAATGCAAAA	GCATCAAGTG	TTTACTCTG	60
AGAAGCGCCT	TGTATGCCCC	GTTACTCTCG	TTCTCCCTCA	GCTCTTGCTT	GTGCTTCTCC	120
ACCTGCCATT	CCACTTTGGC	CTGGTACTGC	CTGTAGTCTT	CCTGGCAGGC	CCCAGTCCA	180
GTTCTTTGGA	GCAGCTGGGC	ATCCAAGAAG	AGGTCATTGC	TGTGGAAGGA	GCCCTCTCGC	240
TCCCTCCCCA	GCCTCTCAAT	CACAGCCAGG	AGCTCTGCCT	GCTGCTGCCT	CTGCTCCTCC	300
ACAGAGCCCC	AGTTGTTGAA	GGCACAGTAC	CTTCTCTCAC	ACTCCCGCGC	CAGGTCTTTC	360
AGGTGTCAGT	TGTCCGTGTT	TGCTACATAG	TCATCCAGGG	CCTGGCCCCG	TCGACGGCCT	420
CTTTGGCCCT	CGAGACA					437

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CCTGCNCNAA	ANNANTCCAA	GCNAANNCCC	AAACAATCCC	AATNCCNACC	CCAAGCTNNG	60
GAGTTCGGCC	CAAAGAGGGC	CCNNCGAACG	TAGATTNCAG	TGAGCCAAGA	TCGTNCCACT	120
GCACNCCAAG	CCNGGGCANC	CAAGAGCGAA	ACTCCGTCNC	CNCNNNANAA	AGAGAAAATT	180
AGCCGGGCGT	GGTGGCGTTA	ATCCCANCTA	CTTGTGAGGN	TAAGGGAGGA	.GAATTGCTTG	240
AACCCAGGAG	GCAGAGGTTG	CAGTGAGCTG	AGATCACGCC	ATTGCACTCC	AGCCTGGGCC	300
ACAAGAGCAA	GACTCCATCT	CCCCAAAAAA	AAAAAAATAG	CGTCAGAAAA	ATGTCCTTGT	360
ATGCCATTTT	CTCCATTTTA	TTGACATTTT	GCCCCACTTT	TGTCCTTGTT	TCAGGGAAAT	420
CGTGGAACAC	ATGGTCCAGC	ACTTTAAAAC	ACAGATCTTT	GGGGATCGGA	AGCCCGTGTT	480
TGACGGCAGG	GTCAACGGCC	TCTTTGNCCC	TCGAGACA			518

## (2) INFORMATION FOR SEQ ID NO:72:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

```

AAACCAAAAC TCATGTTGCT TGNCCCCCA TCGTCGTCTC AAGTGNGGGC GANNACTTTC      60
CTGGTTGGAG CCCTCCGTCC NAACNNCTAA CACAATGTTT TTTCNCAAAC GTTCTACNAA      120
CGCCTGCGAC NAGNCCAGGG AGGGGGTGCT GTGNATCCTC AGCNACGACA CGCTGCAGTA      180
CTGCGACTTC TTGGGCTCCG GGGCGGCCAT CTGGGTCACC ATNCTGTGNA TGGCACGGCT      240
CAAGACAGTC CTGAAATACG TGCTGTTTCT TCTGGGTACA CTGGTCATCT CCATGTCCTT      300
GCAGCTGGAC CGCAGGGGCA TGTGGAACAT NCTGGGGCCC TCCCTCTTTG CCTTCGTGAT      360
CATGGCCTCC ATGTGGGCTT ACCGCTGCGG GCACCGGCGC CAGTGCTACC CCACCTCGTG      420
GCAGCGCTGG GCCTTCTACC TCCTGCCCGG CGTCTCTACG GCCTCTTGN CCCTCGAGAC      480
A

```

## (2) INFORMATION FOR SEQ ID NO:73:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

```

GACCCTCCAN TAATAANCCT TTTGTTTCCC TCGTCNNTGT TNGTCCGTTC CCCTTTCCTN      60
CCCTTGTTTC NNTNTCTGTC ACCAATATTT CCAANCTAAT ACCCAAGCAA NACAATCCNA      120
ACTCCAAGCT CGGGAATTCG GCCCAAAGAG ACCGTAGGCC GAAACCCACC GGANGGAACC      180
ATCTCACTGT GTGTAAACAT GACTNCCAAG CTGNCCGTGG CTCTCTTGGC AGCCTTCCTG      240
ATTTCTGCAG CTCTGTGTGA AGGTGCAGTT TTNCCAAGGA GTGCTAAAGA ACTTAGATGT      300
CAGTGCATAA AGACATACTC CAAACCTTTC CACCCCAAAT TTATCAAAGA ACTGAGAGTG      360
ATTGAGAGTG GACCACACTG CGCCAACACA GAAATTATTG TAAAGCTTTC TGATGGAAGA      420
GAGCTCTGTC TGGACCCCAA GGAAACTGG GTGCAGAGGG TTGTGGAGAA GTTNTGGAAG      480
AGGGCGTCGA CGGCCTCTTT GGCCCTCGAG ACA

```

## (2) INFORMATION FOR SEQ ID NO:74:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

```

CAANTAATAA ANCTTTTGTG TCCCTCGNCA TTGTNNTCGT TCCCCTGTCC NGCCTTGTTT      60
CCNNNGTCCT GCACCAATAT TTCCAAACCN AATACCCAAG CATACAATCC NNACTCCAAG      120
CTNGGAATTC GCCCANAGAG ACCGTCGNGG GAAGAANTTG NCTGGAAACT TGTCATGGT      180

```

GATATATACC	GTCCTCCAAG	AAANGGGATG	CTGCTATCAG	TCTTTCTAGG	AGCCGGGANA	240
CAGATATTAA	TTATGACCTT	TGTGACTCTA	TTTTTCGCTT	GCCTGGGAGT	TTGTGCACCT	300
CCCANCCGAG	GAGCGCTGAT	GACGTGTGCT	GTGGTCCTGT	GGGTGCTGCT	GGGCACCCCT	360
GCAGGCTATG	TNCTGCCAG	ATTCTATAAG	TCCTTTGGAG	GTGAGAAGTG	GAAAACAAAT	420
GTTTTATTAA	CATCATTTCT	TTGTCCTGGG	ATTGTATTGT	CTGACTTCTT	TATAATGAAT	480
CTGATCCTCT	GGTCAACGGC	CTCTTTGGCC	CTCGAGACA			519

## (2) INFORMATION FOR SEQ ID NO:75:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CGGGCCCAAA	GACANGCANN	CCNACAAGAT	GTCGTGTTC	CAAGAAGCTG	ATNGAGGGGT	60
ATCTCGGAAG	CACACGGAAA	CTTTTCCTT	CCTTCAATTC	NACGCACACT	AACCTCTTAA	120
TGAGCAANCG	GTATACGGCC	TTCTTCCAG	TTACTGNAT	GTGAAATAAA	AAAAAGTTG	180
CTGTCTTGCT	ATCAAGTATA	AATAGACCTN	CAATTATTAA	TCTTTTGTTT	CCTCGTCATT	240
GTTCTCGTTC	CCTTCTTCC	TTGTTTCTT	TTCTGCACAA	TATNTCAAGC	TATACCAAGC	300
ATACAATCAA	CTCCAAGCTC	GGAATTCGGC	CNAAGAGGCC	GTCGACCGTT	CGTTATCGGA	360
ATTAACCAGA	CAAATCGCTC	CACCAACTAA	GAGCGNCCAT	GCACCACCAC	CCACGGAATC	420
GAGAAAGAGC	TATCAATCTG	TTGAAGAACA	TGCCCGGCTT	CTTGGTCATC	ATCATGGTGT	480
ACACGNCCTC	TTTGNCCCTC	GAGACA				506

## (2) INFORMATION FOR SEQ ID NO:76:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

TTCCTTGTTT	CCTTTTCCT	NCCCCAATAT	TTCCAAGCTA	ATACCCAAGC	AATACAATCC	60
NACTCCAANC	TCGGGAATTC	GGCCACAGA	GACCGNTGAC	CNTGTAAATG	AGTGAGGCAG	120
GAGTCCCGNG	GAGGTAGTT	GTGTCAATAA	AAATGATTAA	GGATACTAGT	ATAAGAGATC	180
AGGNTCGTCC	TNTAGTGTG	TGTATGGNTA	TCATTTGTTT	TGAGGNTAGT	TTGATTAGTC	240
ATTGTTGGGT	GGTGATTAGT	CGGTGTGTA	TGAGATATNT	GGAGGTGGGG	ATCAATAGAG	300
GGGGANATAG	AATGATCAGT	ACTCCGNCAG	GTAGGCCTAG	GATTGTGGGG	GCAATGAATG	360
AAGCGAACAG	ATTTTCGTTT	ATTTTGGTTC	TCAGGGTTTG	TTATAATTTT	TTATTTTTAT	420
GGNCTTTGGT	GAGGGAGGTA	GGTGGTAGTT	TGTGTTTAAT	ACAAAAAGTT	GGGTCGACGN	480
CCTCTTTGNC	CCTCGAGACA					500

## (2) INFORMATION FOR SEQ ID NO:77:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

```

AACCGGATTC GGNCCNAAAG AGACCGGTTG CCCAAACTT TCTGCTGAGA AGGACATTTT      60
GGAGGGGNTT TGTGGGGCTG AAAAAAGCT GTTCCTGGG AATNNAACCC CCNAGANCTT      120
TCTGAAGAC NTTGAATTAA GATTACCAAN CGATGGGGGA CACAGGAAGG TCCACCCCA      180
NGCTCTGATA TNTGCCATCA CAGTTGCTAC AATCAGCTCT TTCCAATTG GCTACCAACA      240
CTGGGGTCAT CAATGCTCCT GAGAAGATCA TAAAGGAATT TATCAATAAA ACTTTGACGG      300
ACAAGGGAAA TGCCCCACCC TCTGAGGTGC TGCTCACGTC TCTCTGGTCC TTGTCTGTGG      360
CCATATNTTC CGTCGGGGN ATGATCGGCT CCTTTCCGT CGGACTCTTC GTCAACCGCT      420
TTGGCAGGCG CAATTCAATG CTGATTGTCA ACCTGTTGGC TGTCACCTGGT GGCTGCTTTA      480
TGGGACTGTG TAAAGTAGCT AAGTCGGTTG AAATGCTGAT CCTGGGTCGC TTGGTTATTG      540
ACCTCTTCTG CGGGTCGACG ACCTCTTTGG CCCTCGAGAC A                          581

```

## (2) INFORMATION FOR SEQ ID NO:78:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

```

GTCAACCTGG GAGGCTCTCC CCCACCTTCT TTCAATCTCT TCTCAAACCTC TGCATCCTCA      60
GAGGGGCCTT GCCTGATTGG CCTTCTTAAA ATGGATCTGC CCCACCCAC TTTGTACTTG      120
CTGTGCCCTC TGCTTTTCAAG CGTGTCTTCA AACAGGATCT CAACAAGGCC TCCCCTGACC      180
ACACTTAAA ACTGCATGCC CTATATATAC CCCATCTCTC TTATTTTAT TTGTCTCCCT      240
AATGCTTATC CCCAGTATAC TCTGTTTATT GTCTGTCTCT CCTCACTACA AAATAAATC      300
CCCAAGGCCT AGAGTTTTTT CTGTCTTGTG CCTGCTATAT ACCAGTGCTT AGAACAGCGC      360
CCTGCACAGA ATAGAGGCC AATTCAATAT GGATTGCTA CCACTACATC CTATTTGTTT      420
CCTTCCCATC ACTTTTCGAA CACTCATCTA TTCAGCTCTG CTGACCTGTT TCACATCTGG      480
ATCCTGTATA GCAACGTCGA CGGCCTCTTT GGCCCTCGAG ACA                          523

```

## (2) INFORMATION FOR SEQ ID NO:79:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

```

GTNGACTGAT ACTCGAGTAC CTGGATCAGC GGCTGAAAGC TGCAGAGAAC AAGTTTGCCA      60
AGTGCCTCAT GACCTGTCTC AAATGCTGCT TCTGGTGCCT GGAGAAGTTC ATCAAATTCC      120
TTAATAGGAA TGCCTACATC ATGATTGCCA TCTACGGCAC CAATTTCTGC ACCTCGGCCA      180
GGAATGCCCT CTTCCTGCTC ATGAGAAACA TCATCAGAGT GGCTGTCTTG GATAAAGTTA      240
CTGACTTCTT CTTCCTGTTG GGCAAACTTC TGATCGTTGG TAGTGTGGGG ATCCTGGCTT      300
TCTTCTTCTT CACCCACCGT ATCAGGATCG TGCAGGATAC AGCACCACCC CTCAATTATT      360
ACTGGGTTC TATACTGACG GTGATCGTTG GCTCCTACTT GATTGCGTCG ACGGCCTCTT      420
TGGCCCTCGA GACA                          434

```

## (2) INFORMATION FOR SEQ ID NO:80:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

```
GAGGCCCTC AANTTCGCGC ATTTTATTTT ATTTTGTGA NCTGGAGTNT TGCTCTGTAT    60
CCCAGGCTGG AGTGCAGTGG CGCAATCTCG GCTCACTGCA AGNTCCCTCT CCCGGGTTC    120
CGCACATTCT CCTGCCTCAG CCTCCCTAGT AGCTGGGACT ACAGGAGCCC GCCACCACGN    180
CTTGTTAATT TTTTGTGTAT TTTAGTAGA GACAGGNTT CACTNTNTTA GTCAGGATGG    240
TCTCATTNTT CTGANGTCAT GATCCGCCCA CCTCGGCCTC CCAAAGTGCT GGGAKTACAG    300
GMGCGARCCA CCGCGCCCGG CCTATTTTTT GKGGGTTTNA WWTCTGGGTG ACTTGTCAGC    360
AGGAAGTTTT TGTTKTTTTT TTTCCANTGA AAAGATCTGG CCANAATAGT GGGNNTGTCA    420
AAGTATCTCT TTGCAGNTT AATTGTCATT TTCCANTGA CTAAGATGAT GTTGTGCAAT    480
TTTTTCAGAN ACTGTNTGCT ATCTGTATAT CATCTCTTT TTTTITTTTC TTTTGAAGT    540
GGATCCGGTN CGNCCTCTT GCCCTCGAG ACA                                573
```

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

```
GAANCCCCAT CCACTTCNCG GGAGGGGGGA GAGCGCGNG ACGGGTCTCG CTCCTCGGC    60
CCCGGGATTC GGCGGGTGCA GNTGCCGGAT CCTTCAGCGT CTGNATCTCG GCGTCGCCCC    120
GCGTACCGTC GCCCGGCTCT CCGCGCTCT CCCGGGGT CCGGGCACTT GGGTCCACAC    180
GTCTGGTCCT GCTTCACCTT CCCCTGACCT GAGTAGTCRC CATGGCACAG GTTCTCAGAG    240
GCACTGTGAC TGACTTCCCT GGATTGTATG AGCGGGCTGA TGCAGAACT CTTCGGAAGG    300
CTATGAAAGG CTTGGGCACA GATGAGGAGA GCATCCTGAC TCTGTTGACA TCCCGAAGTA    360
ATGCTCAGCG CCAGGAAATC TCTGCAGCTT TTAAGACTCT GTTTGKCAGG GATCTTCTGG    420
ATGACCTGCG GAAGTGATC CGGTTCCGCC TCTTTGCCCC TCGAGACA                468
```

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

```
GAACCGGATC CACTTCCGGG AAAACCTCGG ATTAGCAAGC AATAAAAACA TGACCTCACT    60
CTTCTCAAA GGAGCCCCTG GTCTCCCTG TGTGACTCAG TTCTTTCCAT CTGTTGTCC    120
CGCTGCAAGC CTCTTTCTGC GCTGACTGTG ACATCGGAAC GTGGCCTTCC TGTACCCCC    180
TCCGTGCCAC GCACTGAAGG CCACCCCCC CCACCTGGGA AACTAAGAAC TGGATATTTT    240
GCCTCATTCA CTTGTACTGT AACAAATGTAT ATAATTGGT TGGTATTTC CTATTTAATT    300
TTTAAGAAGC CTATTTTACT AGTGTTTTAT ATGAACAAAG TACTGCAGAA GTTAAACCTG    360
```



TGTTGTATTT TTTCTGAGAT GTTTGTCTTT AAGAGATACT TTTTGCTCAG TTTTATATG 420  
CCAGGAAGTG GATCCGGTTC GGCCTCTTTG GCCCTCGAGA CA 462

## (2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 498 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GGCCCCGATNC ACTTCCGTGG NAAGAGCCTG CAATCCCNCC TACTCAGGAG GCTGAGGCAG 60  
 GAGAATCGCC CGAACCCGAA AGGTGGAGGT TGCAGTGAGC TGAGAATGTG CCACCGCACT 120  
 CCAGCCTGGG TGACAGGGG AGACTCTCTC AAAGTAAATA AATTAAAAA ATTTAANAAG 180  
 ATCATCAAAG AACAAACGAA ATTTGTATT TTCAGTAAGT CAATTTAAAC AATAGAAGCC 240  
 AATTCTACCA CCAGAGGAR CMMATAAAAT CTCATTATTA ATTGAGGGTG GCTTCTCTMC 300  
 CAGGTGRRAA ATTCTATAGR CAGGTATTTT GKTTACTACT GACAGGTAAT AAGATTGTTT 360  
 CTWAGGTAAA GGTAAACCCA GCAACACAAC ATTCTTCACT TTTGTTTAAAT GAACCTCNAN 420  
 ATTCATCATA TTACTTNTAT TTGCTAGCAT GCTTTTGTG GAAGTGATC CGGTCGGCC 480  
 TCTTTGGCCC TCGAGACA 498

## (2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 409 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CGASCCGGAT CCACTTCCCC CTTACGTATC ATTTGTCACA CAGGCCTCAG CCGAAAAA 60  
 AATTCCAGTT TTTGTGATT GCAGTTCCCG TATGCTATTG TCAACCAACA GTTCCGTGA 120  
 TCCTTGAGT CTAATGAGTT TGGATGCATC TATGTTCTTA CTGGATCCAC TGTCCTGCT 180  
 CGGCAGCTCT TCCTCACTGC TGCTACTCTT TTCTGGACAC TCCTTTTTTT CCATTGTCA 240  
 AATGTGGTAT TTATGTCTTT ACTGTATCTT TTTTACCCAT GTGAGTTTCA GGAGCCCCAG 300  
 GGTGCAGGAA GGAGGAGCGG AGGCTTGTTG CTTGGACACT GCCAGGCTGC TCTGTGTTCT 360  
 GTTCCTCTTG GRAAGTGGAT CCGGTCGGC CTCTTTGGCC CTCGAGACA 409

## (2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 611 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GAACCGGATC CACTTCCGAA GAGAAGGTCA GAGCGCACTG CAGGCAGCGC GGCTCTGGGA 60  
 AGAACTTCAC GGAGCCCCCTT CTTAGAGCAG GGAGGGGGCT TTCTCAGTGA AATGTTTGGT 120

TTTCTGCTGC	CTCCTCTGCC	CCAGGCCCCC	CTCCAGGGTA	CTGCCTATCC	CAGATAGGTC	180
AGTGCACCAG	GGACCCGGCC	GCCAGCACCG	CCGACCCCTC	CCAGAGTGAC	GCCCTTGTTT	240
ACTGACAAAG	AGACCTGTCC	CAGGAGTGTC	CTCCACCGAG	CCGGTCAGCT	GTGGGTGGTT	300
TTCTGTGTAC	GACGCTCAGT	AGCCTGTAGC	AATAACAAAC	TCGTGGCTAT	GAATGCAGAT	360
GCAGTGTCT	CATAGAATAA	CTGTTCTGTC	ACTTTTACAG	ACAAATCTAC	GACAAAAAAA	420
AAGATCAACT	TTTTTTTCC	GAACAACAAA	AAAAATGAAT	GATTACAATA	GGAAAGGGAA	480
AAATTAAATA	GCTACATATC	ATTAAACAAAT	TAATGTTCTT	CAAAAAATAC	CTACAAATTT	540
CTCTGTACAT	TCTTTACGCA	CAGCGTAACG	ATGGAAGTGG	ATCCGGTTCG	GCCTCTTTGG	600
CCCTCGAGAC	A					611

## (2) INFORMATION FOR SEQ ID NO:86:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GAACCGGATN	CACTTCCCCT	CCACGTAGTT	GGNAGGGGAA	CCAGCCAACC	CGGCCATAGA	60
TCTCCCCTCG	CCACCAGCCT	TGGTGTCCTT	TCTTGTTAAG	GATCTTGATG	ATGTCACCCCT	120
CCTTGAGCGA	CAGCTCTGAT	CGGTCTCGGG	CGCAGAAGTC	ATAGCGGGCT	TTGGGTGTGC	180
CAAAATACTT	TGTGCTTCCC	ACTGNTGGNC	TGCTGATGGT	TCTCTTTTCA	NGCTCCTTGA	240
AGGGGAACCTG	CAANGTGGTG	TCCAGAGACT	TGAAGCAATC	CNTTAGAGAG	TTCTGNTGGT	300
AAAACCTCCAC	CAGNTCCGTA	AGCCCCCNGA	AAGNCTTTTT	CTCTGTGATC	CGGTACAGAA	360
CCTTCTTCTG	TCA					373

## (2) INFORMATION FOR SEQ ID NO:87:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 489 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GTTGACCGCC	CACGATGATC	TTGCCGCCAC	GCTTGCTGGT	CTTCTCCACT	GACAAGGCAC	60
TGCTCAGGCC	CTGCTCATGC	TTCCCCAGAC	CCTGGCCCTC	CCGGAAGCCG	NACTTCTGCA	120
TGATCTTGTTG	CGCCACCGTG	CCCCCATGT	TAGCGAGGAA	GGAGTTGCTA	GGTCCGGTTG	180
GAGATCTCGG	TCTGTCTTGT	TCCTCGTACA	CTGGGGGAGG	AATGGCTGCT	TTGGAAGACT	240
GTGATCGAGG	TCTTGAGTCC	TCTTCATAAG	GAAAATCTCG	GGGTAACCTT	TTGTCTTTCT	300
CTACCAGAGA	AGTGGGTGGG	GCAATGGCAG	CTCCGCCCAT	ACTTCTCTTC	CTCCTCTCTC	360
GCTCATAATC	TTCATCTTCA	TCAGAATCTG	GATCTGGTCT	CCTTGCAAAC	CCACTTGCTT	420
CATGTCTGTC	TTTACGCCTT	TTTCCCTTT	CTTCTATTTT	CGTCGACGGC	CTCTTTGGCC	480
CTCGAGACA						489

## (2) INFORMATION FOR SEQ ID NO:88:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 520 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

```

GACGACTTTG TGGGTATTAA TTTTGTGTTA AGTTTAAAAT AAAAGTAAAG ATTCAATTTG      60
GATATCAGTT GAAACCCCTT AGTAACTCAG TTTCTGTTAT TCTTGTTCTC ATTTCCCTTA      120
AATACACTTG TTCTTGGCTT TTGCCATTTT GATTCTGTGA AGTAGGCAGG AGCAGGGATT      180
AATTTATACA GTATTCCTGT TCTGAACAAA ACCAGAAAAG TCACTGTATA AACTTGACTT      240
AAAATAGTAT CTTTCTCTTY TCATGTATTT TCATTTGGGG GAAAAAAAAT CTCTTTAATT      300
GTAACCTGAA TTCAAGCTGT ACCCTCCCAT GGTCTACAC TCTAGAGCTA ATCTGGTTGG      360
GCAGAAAGGC AGAAGGATGG TATATTGTCC CATTGTGCCT ATAATGTATT TTAAATTGGT      420
CATTCCACCT TACCTAATGG AAATTCTTGC AGCTTTCCTA GTGCTCATCA GCGGTTTAG      480
GAATTCACCTA ACGTCGACGG CCTCTTGGC CCTCGAGACA      520

```

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

```

GTTGACGGCG TGGTGGCGGG TGCCTGTAAT TCCAGCTACT CAGGAGGCTG AGGAAGGAGA      60
ATCATTTGAA CCTGGGAAGT GGGGGTTGCA GTGAGCCAAA ATCGTGCCAT TGCACTCCAG      120
CCTGGGCAAC AAGAGTGAAA CTCCATCTCA GAAAAAAAAA AAAAAAAAAA AAAAAAAAAAG      180
GAAGGAACCG GTGGGGCAAG CAGAGTTAAG ATGCTTTGCT AAGTTAAAAA GTCTACTAAC      240
TACCAAATCT TGCTGTGGYT TATCCAGAGC TCTCAAAATG CTGCCAATCT ATTTTAAAGA      300
AGACCTAAAT CCTCATTG GCTTTTAGGA CACTAGGATT TGCCTTCAAC CCATGTCTCC      360
AGTCATATAT TTTCTTACTA TTCTTCAAC ATACCTTTTT CTCTTTTCTT CACTCTTCAT      420
TATGCTGTTT AAATCGTCGA CGGCTCTTT GGCCCTCGAG ACA      463

```

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

```

GTACAAGAAG TGGTCCATTC CTTTGTCTGA AGGAGCGACA GGAGCATCTA CGGTTGAGAA      60
GACAGAAAGT TTGGCTTCGT CGATGTCTTG CTGTGTGAAT TTCCAGACT TAGCCCAGTC      120
GACAGCCTTC CAAAAGACT GGAGCGTCTC TATTGTATTT GGTCCCTGT AAGAGTAAAC      180
GGTGAAATC CCATTGTGGC TGAGTTTTCG GCCTCCACCA TAAGCACCGC CTTTTCTCG      240
AATTTCTGTA TGCAAGAATT TGGCAGTCAT CAAACGTGCA AGGATTTTAA GACTGGCATG      300
ATCTGGGTCC GTGTAGGGGA CAGTTCGGAT GCATTACCC ACGTTATTCA CCGGGAAGGG      360
CATCAGGAAG TGAGTCTTCA TCTGCCAGGG CTTGAAGGTG GGTTCATGA CCAGCTTCCT      420
AATGACCTGG GAGCCATGGG GAACGTGGG ATCTCCACCA GAGCTGCTGG GCACAGGTTT      480
CTCGACCGTG TGTGGGCGCA CAGGCCGTCG ACGGCCTCTT TGGCCCTCGA GACA      534

```

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 450 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

```

GTCGACCAGG ACTAGATTCT GTCTCTCCAA AGTGGCCCCA GCCCTGTTCT CTGTACTAGG      60
GAAGCCAGCT GTGTCTTTTC GAGGACAGTT GGTCCAGCCA GCAGGCTCAG TTCAGATACC      120
AGACAACCAT TCCAGCACGA GGGCTCAGCG CCTGGCCCCC GGCGGTCGCT CCAGTGCCTG      180
TGTGCCCCACC AGCACATCCA TGAGGTAGTC CAATTCGGCC TCGTCCAGCT CCGGAGCTTC      240
CTCCTTGGCC GGCCCATCCT CAGGGCCTGG TTTGAGGCCC TCAGAGGCTG GTGCCCCAAG      300
TTCATTGTCA TACATAGAGG TGTCAATATC CTCAAACAGG CCCTCAAGCC CATCGTCCAG      360
TAGACAGCCA GTGGCTGGGC CCAGCAGGTC CAAGGCACCC AGGCTGGGCG CTGCTCCCCC      420
GATGCTACGG CCTCTTTGGC CCTCGAGACA      450

```

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 449 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

```

GTCGACGGCG GYCATGGCAA AGCAGTACGA CTCGGTGGAG TGCCCTTTT TTGTGATGAA      60
GTYTCCCAAA ATACGAAGAA GCTCGCCAAG ATCGGCCAAG GCACCTTCGG GGAGGTGTTT      120
AAGGCCAGGC ACCGCAAGAC CGGCCAGAAG GTGGCTCTGA AGAAGGTGCT GATGGAAGAC      180
GAGAAGGAGG GGTTCCTCAT TACASCCTTG CGGGAGATCA GGATCCTTCA GCTTCTAAAA      240
CACGAGAATG TGGTCAACTT GATTGAGATT TGTCGGAACC AAAGCTTCCC CCTTATAACC      300
GCTGCAAGGG TAGTATWTTA CCTGGTGTTT GACTTCTGCG AGCATGACCT TGCTGGGCTG      360
TTGAGCAATG TTTTGGTCAA GTTCACGCTG TCTGAGATNC AAGAGGGTGA TGCAGATGCT      420
GCTTAACGGC CTCTTTGGCC CTCGAGACA      449

```

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 493 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

```

GTCGACAAAA CATGGAGTTG TTCCTTTGGC CACATATATG CGAATCTATA AGAAAGGTGA      60
TATTGTAGAC ATCAAGGGAA TGGGTACTGT TCAAAAAGGA ATGCCCCACA AGTGTTACCA      120
TGGCAAAACT GGAAGAGTCT ACAATGTTAC CCAGCATGCT GTTGGCATTG TTGTAAACAA      180
ACAAGTTAAG GGCAAGATTG TTGCCAAGAG AATTAATGTG CGTATTGAGC ACATTAAGCA      240
CTCTAAGAGC CGAGATAGCT TCCTGAAACG TGTGAAGGAA AATGATCAGA AAAAGAAAGA      300
AGCCAAAGAG AAAGGTACCT GGGTTCAACT AAAGCGCCAG CCTGCTCCAC CCAGAGAAGC      360
ACACTTTGTG AGAACCAATG GGAAGGAGCC TGAGCTGCTG GAACCTATTC CCTATGAATT      420

```

CATGGCACAA TAGGTGTTAA AAAAAAAAAA TAAAGGACCT CTGGGGTCAA CGGCCTCTTT 480  
GGCCCTCGAG ACA 493

## (2) INFORMATION FOR SEQ ID NO:94:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

GTCGACGAGG GGGTCATGGY AGGCAGGGGC AGGTGCGTCA GAGATGGAGC GCAGGTCCTG 60  
CATGGAGAAG CTCGCGAGCC TGCCGGCCAG CGCCCCCTGA CTCTTGGTGG CAGCCTGCAC 120  
AGCAGCGGAG GCGGCAATGT TGAGGCCCCG CTTCCCGAAG CTGAGCACGG TCTCGTAGCT 180  
GCGCTCCTTG GCCTGCACGA TGTACGCGTC GATCTCCTTC TCATGGCGGG ACAGGGACGG 240  
GTGGACAAAC TTGCGGTAAA GCAGGCTGGC GCCCTTGGTG TAGGGTGAGA GCAGCCACAG 300  
CACGAAGGCC ATCTTGATCT CATAGTAGAA AGGGAACCAG GAGATAAAAA TGTCTGTAAC 360  
GATCTCTGCT GCCATGAAGA GTGCARCAA CTATCCAGTA CATCATCCAG TGGACGGCCT 420  
CTTTGGCCCT CGAGACA 437

## (2) INFORMATION FOR SEQ ID NO:95:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GTCNACCGCC CTTCTGTCT CCTCCTCAGT NGTACACCTG TGTGGTCTCC ACCACCTCAG 60  
ACTTNTCTCCG CCCCTTTCAG TNGGAAGAAG GNGCAGGCCG GTCTCGGGT CCTCCACGCA 120  
CCGNTCCAGA AGTTGCCTGT ACGTGAGGTT CTCATGCGTG TTGGGGTNAA AGAAGCCCTT 180  
GGTGTCTGTCG CTGGGGTCCG CCGGGACGCG GKTCATCTCC TCACTGAAGT AGCCCCGCTG 240  
GTAGRSCACG TCCACAGACA CGCGGTGTT GTGYACGGGG TCGATGATRC CGCCCGTGGC 300  
GATCTGGGCC TCCAGNAGGN GGATNCCGTG CTGCNGGAGA ACCAGNCCCT TCTNNATGTC 360  
CTGGAAGAGN GAGATGGTCC CCCCCAGTA GGGGTCTCTG TANCCGGTGA CGNCCTTCTC 420  
GACAGACAGC ATCTGCTCGT GAAGCTCGGG GCCCACCACG CCCGCCTTCA CGGCCTCTTT 480  
GGCCCTCGAG ACA 493

## (2) INFORMATION FOR SEQ ID NO:96:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GTTGACCCAC GTTAGTACGG TTGGATAGGA TATGCTCTCA TGGTAACGG TCCAAGTTGG 60

```

AATGGTCTTC CAGTCTCCAT GGNATCCACA TGCTACTGGC GTTAGTTCCA GATCTTGAGG 120
AAGNTATCCC AGGACCCTGT CGCCACAGGC ATGNCATCGT CANTCACGCC CAGGCAGCTG 180
ACGCGGTTGT CATGNCCAGN CAAGACAAC GCGCGGTCGG GTTTGNGTGC ATCCCAGACG 240
TTGCAGTTGA AGTCGTCGTA CCCAGCAAGG AGGAGGSGSC CGCTCTTGGW GAAGGAGACA 300
GAGKTGATCC CCCAGATGAT GTTGTCTATG GAGTAAGTCA TGAGCTCCYG GTCAGCACGA 360
AGGTCAAACA CCCTGCNNGT GCGCTCGTCT GAGCCAGTGC CAAATGCATT GCCATTTGGA 420
AAGAANCAAA TGNCAATTGAT GTCAGACTCG TGCCCAGTGA AGGTCTNCCG GCACATGCCT 480
TCTCGCACAT CCCAGAGTTT GTCTGAAGCA TCACAAGCAC CAGAGACGAA CAGTCTGGTG 540
TCAGTCGACG GCCTCTTTGG CCCTCGAGAC A 571

```

## (2) INFORMATION FOR SEQ ID NO:97:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

```

GTCGACGTAC CACCAGCAAC CATCAATCCC GTCTCCTCCT GCCTCCTCTC CTGCAATCCA 60
CCCCGCCACG ACTATCGCCA TGGCAGCCCT GATCGCAGAG AACTTCCGCT TCCTGTCACT 120
TTTCTTCAAG AGCAAGGATG TGATGATTTT CAACGGCCTG GTGGCACTGG GCACGGTGGG 180
CAGCCAGGAG CTGTTCTCTG TGGTGGCCTT CCACTGCCCC TGCTCGCCGG CCCGGAAC TA 240
CCTGTACGGG CTGGCGGCCA TCGGCGTGCC CGCCCTGGTG CTCTTCATCA TTGGCATCAT 300
CCTCAACAAC CACACCTGGA ACCTCGTGGC CGAGTGCCAG CACCGGAGGA CCAAGAAGTG 360
CTCCGCCGCC CCCACCTTCC TCCTTCTAAG CTCCATCCTG GGACGTGCGG CTGTGGCCCC 420
TGTCACCTGG TCTGTCTCTT CCCTGCTGCG TGGTGAGGCT TATGTCTGTG CTCTCAGTGA 480
GTTCTGTGGC CTTCTCTCAC TCACGGCCTC TTTGGCCCTC GAGACA 526

```

## (2) INFORMATION FOR SEQ ID NO:98:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 520 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

```

GTTGACTTTG TGGGTATTAA TTTTGTGTTA AGTTTAAAT AAAAGTAAAG ATTCATTTTG 60
GATATCAGTT GAAACCCCTT AGTAACTCAG TTTCTGTTAT TCTTGTTCTC ATTTCCCTTA 120
AATACTAGTT TTCTTGCTT TTGCCATTTT GATTCTGTGA AGTAGGCAGG AGCAGGGATT 180
AATTATACA GTATTCCTGT TCTGAACAAA ACCAGAAAAG TCACTGTATA AACTTGACTT 240
AAAATAGTAT CTTTCTCTTT TCATGTATTT TCATTGGGG GAAAAAAAT CTCTTAATT 300
GTAACCTGAA TTCAAGCTGT ACCCTCCAT GGTCTACAC TCTAGAGCTA ATCTGTTGG 360
GCAGAAAGGC AGAAGGATGG TATATTGTCC CATTGTGCCT ATAATGTATT TTAAATTGGT 420
CATTCACCTT TACCTAATGG AAATTCTTGC AGCTTTCCTA GTGCTCATCA GCGGTTT TAG 480
GAATTCACTA ACGTCGACGG CCTCTTTGGC CCTCGAGACA 520

```

## (2) INFORMATION FOR SEQ ID NO:99:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

```

GAATTCGGCC AAAGAGGCCG TTGACGGGGC TGGAGGAGGA AGAAGAGGTG GATCCCCGGA      60
TCCAGGGAGA ACTGGAGAAG TTAAATCAGT CCACGGATGA TATCAACAGA CGGGAGACTG      120
AACTTGAGGA TGCTCGTCAG AAGTTCCGCT CTGTTCTGGT TGAAGCAACG GTGAAACTGG      180
ATGAACTGGT GAAGAAAATT GGCAAAGCTG TGGAAGACTC CAAGCCCTAC TGGGATGCAC      240
GGAGGGTGGC GAGGCAGGCT CAGCTGGAAG CTCAGAAAGC CACGCAGGAC CTCCAGAGGG      300
CCACAGAGGT GCTCCGCGCC GCCAAGGAGA CCATCTCCCT GGCCGAGCAG CGGCTGCTGG      360
AGGATGACAA GCGGCAGTTC GACTCCGCCT GGCAGGAGAT GCTGAATCTC GCCACTCAGA      420
GGGTCATGGA GCGCGAGCAG ACCAAGACCA GGAGCGAGCT GGTGCATAAG GAGGTCGACG      480
GCCTCTTTGG CCCTCGAGAC A                                     501

```

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

```

GTCGACCGTG TCCAGAGCCC ACCTCCCTCA CACCCACACA GCGCTTCCTA AAGGCAGGGA      60
CAGGAGCTGG CCTCCCTCGC CTGCTGGCAT GGGGCTGGAC ACAGGAGGAA GTGGCGTGGG      120
GGCTGCCTGA GGGGAGTGAG GCGGCAGGAT AGCTTCCCCA GCAGGTCTCT GGCTCAGGTC      180
CAGGTATCTC CTCCTCCCCA TACCTCTGCC TCTCGCCTCC GCTCAGAAAA GCAGGTGCCC      240
TTAAGAGCCA TCTCCACCCC CATGTAAACT GCACACAGGA AGGGAGAGGC CACTCCGACT      300
GCTCTGAGGT CCAGGTAGGA TGGTTTCCCC CAGTGTCTGG GTGGGGAGCA AGGAACTCCA      360
GGGGCGACCT TGTGCCACCG CATCACCTTC CTGCTCAGGG AAGGGGCCCC TGCTGCCGCT      420
TGGAGGGTGC CATGCCCAGA GCCTCTGCCC CTAGCCTCAG CCTCGCCTAC TCCTGGGGGG      480
CTCCAGCACC CCCGGCCGTC AACGGCCTCT TTGGCCCTCG AGACA                     525

```

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

```

GTCGACGCGA GTGGAGACCT GTGGTAGAGA AGCTCCTTTT GATGTCCTAC AGGCTTTCCA      60
CTGTGGTGTC TCCAGTCATT CAGAGCTCAT CCCCTGAAGG CCTCATCCCA ATGGACACTG      120
ATTGAGAGTC AGCAASCCGC TTACAGATGA TTCTGAATGA GATTCANCCT CGAGATACTA      180
ATGATTATTT TAACCAAGCC AAAATATTGA AAGAACATGA TAGCTTTGAT ATGAAGGACT      240
TGAATGCTAG TGTGGTGAAT ATTGATACTT CTACAGAAAT CAAAGGTAAA GAAGTAAAAA      300
CATGTGATGT AACTGCGCAG ATGGTGCTGG TATGTTGTTG GAGAAGTATG AAGGAAGTTG      360
CTTTACTTTT AGGCATGTTG TGCCAGCTTC TGCCCATGTC AACGGCCTCT TTGGCCCTCG      420
AGACA                                     425

```

## (2) INFORMATION FOR SEQ ID NO:102:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

```

GGGACGTAAT CAACCCAAGC TTATGACCCG CACTTACTGG GAANTCNTCG TTCATGGGGA      60
AGAANTGCAA TCCCCGATCC GCCATCACGA ATGGGGGGCA CCGGGTTANC CGCGCCTCCC      120
GGCGTAGGGT AGNCACACNC TGANNCAGTC AGTGATATCGC GCGTGCAATC CCGGACATCT      180
AAGGGCATCA CAGACCTGTT NTTGNTCAAT CTCGGGTGGN TGNNCGCCAC TTGTCNCTCT      240
AAGAANATGG GGGACGCCGC CCNCTCGGGG GTNGCGTAAC TAGNTAGNAT NCCAGAGTCT      300
CGTTCGTTAT CGGAAGTAAC CAGACANATC GCTCCCCCAN CTAAGANNNG CCATNCACCA      360
CCACCCACGG AATCGAGANA GAGCTATCAA TCTGTTGTTA GGACATGCCG GGCTTGCTTG      420
GTCATCATCT TGGTGACNC GACCTCTTTG NCCCTCGAGA CA                          462

```

## (2) INFORMATION FOR SEQ ID NO:103:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

```

GTCGACAGAA ATCATTATTC TTTATTTGCA GNCATTCCAC CCCACCTATG TTTTCTTCTC      60
CTTCCTTCTT CTCTGTCAGG AGAGTTCTTG TCATGCTGAG CTTCTTCATT GTATGGCATT      120
TATATTTTAG CACTGTTTTA TTATTGCCCT CTGTATCAGC ATGTTCAACA TTTTCTTCAA      180
ATATAACACA GGTCCCTAGA GTGTCTTCAT ACTCCCCAGC AAAGACACAG CTGTCCACTT      240
GCAGAATGGG CCTCTCAGTG TCAATGCCCA AAACCTTGCA TTTATTTTCA CATTTTGAGA      300
GGAAGTCTGA ATCAATAATT CCTGATAATT CCACCAGAAC CAACTGCTCC TCCTCTTCCT      360
CGTCTTCTCC GTCCTCTGGA CTCGCTCGT CCGCCGCCGC CGCCATGGTC CCGCGGCGGT      420
TGACGGCCTC TTTGGCCCTC GAGACA                          446

```

## (2) INFORMATION FOR SEQ ID NO:104:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

```

GANTTCCAGT GAAGTTGCCT TTTTGCCNNC CCTAGNCATC CAACCTINTC AAAACCAAGT      60
ANACNAGGCT GATTCTGGAA GTTCTTGAGG AAAAAGCAAG CTTTACAACC AAAATACCCA      120
GATGCTGTGN CCACATGGCT AAACCCTTGA CCCATCTCAG AAGCAGAATC TCCTANCCCC      180
ACAGAGTGCT GTGTCCTCTG AAGAAACCAA TGACTTTAAA CAAGAGACCC TNCCAAGTAA      240
GTCCANCGAA AGCCATGACC ACATGGATGA TATGGATGAT GAAGATGATG ATGACCATGT      300

```



GGACAGCCAG GACTCCATTG ACTCCANCGA CTCTGATGAT GTAGATGACA CTGATGATTC	360
TCACCACTCT GATGAGTCTC ACCATTCTGA TGAATCTGAT GAACCGGTCA CTGATTTTCC	420
CACGGACCTG CCANCAACGT CGACGNCCTC TTTGNCCCTC GAGACA	466

## (2) INFORMATION FOR SEQ ID NO:105:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 568 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GTCGACAGCG ACCGCTCCTC CCTTCCTTCC TTGAATCAGA GCACGGTAGA AAGCTGCTGC	60
TCTATGCCGA AGTGTTCGGA AATTCTTGGC AGCTGCATAG ACCGCGGGGC TGTCCTCTAA	120
CCTTTGCTCT TGTGCGCTCC TCCACCAGGA GGGCCCCCCT CCCTGTACCC CAGCTTCCCA	180
CAGAGCTGCA GGCACAGCTT GGCTGCCTCC CGCTTCCAGA CCCCTATCTC CATCAGGTGG	240
GCCTGAGGCG GGGCTGACTC TTTCTTTAGG CCCCTCACAG GGACTAGAGC AGAATGGCAC	300
TCAGTAAGCA GGGGTGACAA CTAGAGGAAT GGCAGGGTGT GTTCAGCTGG GAGAACAGTT	360
ACCAGAGACG CTGTGATTCT TCAGGTGTGA GGGCAACTGT TACAAGACTT AAGTAGCAAC	420
AACAACCATG GTAGACGCTG CCTTCGATTG TGCCCTTGGG AGTCCCAGGC CTGGCACCAG	480
GCCCTACTCA TCCTTCATTT CTTTTCTTT TCTTTGTTT TTTGTTTTT GGGTTTTTG	540
GTCAACGGCC TCTTGGCCC TCGAGACA	568

## (2) INFORMATION FOR SEQ ID NO:106:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GATTCANTTT GGATATCAAG TTGNCNCCCC CNTAGTAACT CAGTTTCTGT TATTCTTGTT	60
CTCANCTTCC CNATAAAAAC ACTTGTTTCTG GGTNTTGCC ANNTTGATTC TGTGAAGTAG	120
GCAGGAGCAG GGATTAATTN ATANAGTATT CCTGTTCTGA NCGCAACCAG AAAAGTCACT	180
GTATAAACTT GACTTAAAAT AGTATCTNTC TCTTTTCATG TATANTCAGG TGGGGGGGNA	240
AAAATCTCTT TAATTGTAAC CTGAANTCAA GCTGTACCCC NCCATGGTCC TAACTCTAG	300
AGCTAATCTG GNTGGGCAGA AAGGCAGAAG GATGGTATAT TGTCCCATG TGCCTATAAT	360
GTATNTTAAA NTGGTCATTC CACCTTACCT AATGGAAATT CTTGCAGCTT TCCTAGTGCT	420
CATCAGCGGT TTTAGGAAGT CACTAACGTC GACGGCCTCT TTGGCCCTCG AGACA	475

## (2) INFORMATION FOR SEQ ID NO:107:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CCTGAGTTGT	GTCTAAGGNN	CNCAAGACAA	GTACCCAAGT	TTCCTCTAGN	TNTTCTCTTT	60
AAGCTTCTCN	AGTCATACAT	TTNCAAGCGT	CCTTTTGTCA	ACCATNCCAG	TCNANATACA	120
TTATTTGTCC	TCCAATGGNT	GACTTGCCAG	CATCTACGTG	NCCAATGAAT	ACTACATTTA	180
CATGCTCTTT	CTTAGGAGCA	CCTGGCGGTG	CAACCACAGA	CTTAGGTNTT	GGGATTTCTT	240
CTTCCTCCTC	CATCATTTC	TGGGCACTTT	TCTCTGGCGG	CCTTCCATCT	CCCAAGGAAC	300
CACCCCTGG	CTCTGCTTCA	CTTATTTCTT	CTTTGTGCTC	CCATGATTCT	TCTGGAGACA	360
TTTCTGTCTC	TCCACTTTCT	ACAATAGGTT	CTGAAAGTTC	CATGCTAACA	GCTGAATTTG	420
AACCTTCACA	CAATGACTGT	TCGTCGACGG	CCTCTTTGGC	CCTCGAGACA		470

## (2) INFORMATION FOR SEQ ID NO:108:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GAATTCGGCC	AAAGAGGCCT	ACTCACAGTC	ATCAATTATA	GACCCACAA	CATGCGCCCT	60
GAAGACAGAA	TGTTCCATAT	CAGAGCTGTG	ATCTTGAGAG	CCCTCTCCTT	GGCTTTCCTG	120
CTGAGTCTCC	GAGGAGCTGG	GGCCATCAAG	GCGGACCATG	TGTCAACTTA	TGCCGCGTTT	180
GTACAGACCC	ATAGACCAAC	AGGGGAGTTT	ATGTTTGAAT	TTGATGAAGA	TGAGCAGTTC	240
TATGTGGATC	TGGATAAAAA	GGAGACCGTC	TGGCATCTGG	AGGAGTTTGG	CCGAGCCTTT	300
TCCTTTGAGG	CTCAGGGCGG	GCTGGCTAAC	ATTGCTATAT	TGAACAACAA	CTTGAATACC	360
TTGATCCAGC	GTTCACCA	CACTCAGGCC	GTCGAG			396

## (2) INFORMATION FOR SEQ ID NO:109:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GAATTCGGCC	AAAGAGGCCT	ACCCGATTGC	TAAATGGATT	ATGAAAGCAA	ATTGCTACTG	60
GGAGGTGATG	GTCAAAAGCA	AACCTAGATG	GTTTTCACAC	CATCTGTCAT	CATGACTCAA	120
AGGGAAATGC	TAGCCACACC	ATTTTCCAGT	GAAGCCACTG	CTTTACACAG	AAGATACACA	180
TAGCTTCCTA	TTGTTATTTT	CTTTTCTAAT	TATGTACATT	TAGAAAAAAA	ATACAACACT	240
GTGTAAACA	GCAGGACAGC	TAGCAATGGA	ACATACAACA	CTATGCTGAA	AAACCACAAC	300
AGCTTGTTA	AGCGGAGGAG	AGAAACAGAG	ATGGCCTTCA	TGGAGTGAAG	CTGTCAATGC	360
CTGCCATCTC	CTTAGTCTGT	GACGGATCTG	CACTCTGAGG	GCAGGCCTTC	TGAGCGCCGC	420
CACTTTGCCA	GGCGCTGCTT	AAACCATTTC	TGGGTCTCCT	CCTCGGAAAG	GCCTGCCTCG	480
GCCGCGATGA	GGCACAGCGT	GGTGAATCC	GGGTGCTTGT	CGAG		524

## (2) INFORMATION FOR SEQ ID NO:110:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GAATTCGGCC AAAGAGGCCT ATTTTTTTTT TCTTTTTTTA GGCATATGTA GTAATATTAG	60
AAACATTTAA TTTGGGAAAC TTTGATTCTT GAAAGAGAAA ACAAAGCAT GTGAATAAAC	120
TTTGAAGTGT TCACCTCAGT TTGGGACCAA ACTGCTTGGA TCTTTGTAAA AACCGGTTTT	180
GTATGTCAAG GAGGAGTTTA AGGCCTTTCC GACCACCTG TGTTCCTT TTCTGCCGAG	240
CCATGTATCA CGTGGAGTTG CTCCTTACCA CACCTCACGT GCCCCTGAGC CCTATTTCCT	300
GATTCTTCT GGGCTGGACT TCCCCGTTCT CCACCAGCAG CTCCAGTATC CCTGTTGAAT	360
TCTAGACCTG CGTCGAG	377

## (2) INFORMATION FOR SEQ ID NO:111:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GAATTCGGCC AAAGAGGCCT AGCGGACAAG TTTGAGAGAC CTGGCCTTGG CCAAAGCCCT	60
CGATTGCTG TGTCAGAAAA ACTGAGGTGA GAAGAGACCA CCACCCTCTC CACCACCCTC	120
TCAGTAGGAA AGCGGGATCA ACAGAGATCA GAAGGACAGC ACACTCACAC CTGCACATGA	180
ACACACCATC TATGTCAGGA AATCCAGGGG AAGGGGAAGA GGGGTGGAGT GGCTCCGCAG	240
GGCTGACCTG ACAGGGGACA GGAACACTCC CCTAGACCCA GGAAGTCGC CCCAAATCCA	300
AAGCTCTTGA AAGGAGGTAT GGCCTCGAAA CTCCAGAAGC CTCTTCTGCC AACGCACCGA	360
GGACCTGCAC CTCCCATTCG GCACGCGTCG AG	392

## (2) INFORMATION FOR SEQ ID NO:112:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

CAATTCGGCC AAAGAGGCCT ACAGCATTTC TACTCCTTCC AAGAAGAGCA GCAAAGCTGA	60
AGTAGCAGCA GCAGACCAG CAGCAACAGC AAAAAACAAA CATGAGTGTG AAGGGCATGG	120
CTATAGCCTT GGCTGTGATA TTGTGTGCTA CAGTTGTTCA AGGCTTCCCC ATGTTCAAAA	180
GAGGACGCTG TCTTTGCATA GGCCCTGGGG TAAAAGCAGT GAAAGTGGCA GATATTGAGA	240
AAGCCTCCAT AATGTACCCA AGTAACAACT GTGACAAAAT AGAAGTGATT ATTACCCTGA	300
AAGAAAATAA AGGACAACGA TGCCTAAATC CCAAAGTCGA G	341

## (2) INFORMATION FOR SEQ ID NO:113:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

GAATTCGGCC AAAGAGGCCT AGCAGTAGCA TGTGCAGCAA CCAATCAAGA TGGAGAACTA	60
TACCTGCACT CATTGTGTG TTTGCATGTA TAGTTCTCTG CAGTAGCATG TGCAGCAACC	120
AATCAAGATG GAGAACTGTT CCATCGCAAA GCTCCCTCTT GCCACTTCTT TTTAGCCACC	180
CAATCCTCTC TGCTCCCGTC GAG	203

## (2) INFORMATION FOR SEQ ID NO:114:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 585 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GAATTCGGCC AAAGAGGCCT ATGAAGATCA GCTATTAGAA GAGAAAGATC AGTTAAGTCC	60
TTTGGACCTG ATCAGCTTGA TACAAGAACT ACTGATTTC AACTCTTTGG CTTAATTCTC	120
TCGGAAACGA TGAAATATAC AAGTTATATC TTGGCTTTTC AGCTCTGCAT CGTTTTGGGT	180
TCTCTTGGCT GTTACTGCCA GGACCCATAT GTAAAAGAAG CAGAAAACCT TAAGAAATAT	240
TTTAATGCAG GTCATTCAGA TGTAGCGGAT AATGGAACTC TTTTCTTAGG CATTTTGAAG	300
AATTGGAAAG AGGAGAGTGA CAGAAAAATA ATGCAGAGCC AAATTGTCTC CTTTACTTC	360
AAACTTTTTA AAAACTTTAA AGATGACCAG AGCATCCAAA AGAGTGTGGA GACCATCAAG	420
GAAGACATGA ATGTCAAGTT TTTCAATAGC AACAAAAAGA AACGAGATGA CTCGAAAAG	480
CTGACTAATT ATTCGGTAAC TGACTTGAAT GTCCAACGCA AAGCAATACA TGAACTCATC	540
CAAGTGATGG CTGAACTGTC GCCAGCAGCT AAAACAGGGG TCGAG	585

## (2) INFORMATION FOR SEQ ID NO:115:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GAATTCGGCC AAAGAGGCCT ACTGGCGGCC GCGGAGACGC AGAGTCTTGA GCAGCGCGGC	60
AGGCACCATG TTCCTGACTG CGCTCCTCTG GCGCGGCCGC ATTCCCGGCC GTCAGTGGAT	120
CGGGAAGCAC CGGCGGCCGC GGTTCGTGTC GTTGCCCGCC AAGCAGAACA TGATCCGCCN	180
CCTGGAGATC GAGGCGGAGA ACCATTACTG GCTGAGCATG CCCTACATGA CCCGGGAGCA	240
GGAGCGCGGC CAGCGCGCGG TGCGCAGGAG GGAGGCCTTC GAGGCCATAA AGGCGGCCGC	300
CACTTCCAAG TTCCCCCGCG ATAGATTCAT TGCGGACCAG CTCGACCATC TCAATGTCTGA	360
G	361

## (2) INFORMATION FOR SEQ ID NO:116:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GAATTCGGCC AAAGAGGCCT AAACAAATG GTTATCAACC ACTTGGAGAA GTTGTGTTGTG	60
ACAAACGATG CAGCAACTAT TTAAAGAGAA CTAGAAGTAC AGCATCCTGC TGCAAAAATG	120
ATTGTAATGG CTTCTCATAT GCAAGAGCAA GAAGTTGGAG ATGGCACAAA CTTTGTCTG	180
GTATTTGCTG GAGCTCTCCT GGAATTAGCT GAAGAACTTC TGAGGATTGG CCTGTCAGTT	240
TCAGAGGTCA TAGAAGGTTA TGAAATAGCC TGCAGAAAAG CTCATGAGAT TCTTCCTAAT	300
TTGGTATGTT GTTCTGCAAA AAACCTTCGA GATATTGATG AAGTCTCATC TCTACTTCGT	360
ACCTCCATAA TGAGTAAACA ATATGGTAAT GAAGTATTC TGGCCAAGCT TATTGCTCAG	420
GCATGTCGAG	430

## (2) INFORMATION FOR SEQ ID NO:117:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GAATTCGGCC AAAGAGGCCT AGAAGAAGAT GATCCTAAAC AAAGCTCTGA TGCTGGGGGC	60
CCTCGCCCTG ACCACCGTGA TGAGCCCTTG TGGAGGTGAA GACATTGTGG CTGACCACGT	120
TGCCTCTTAC GGTGTAAACT TGTACCAGTC TTACGGTCCC TCTGGCCAGT TCACCCATGA	180
ATTTGATGGA GACGAGGAGT TCTATGTGGA CCTGGAGAGG AAGGAGACTG TCTGGAAGTT	240
GCCTCTGTTC CACAGACTTA GATTTGACCC GCAATTTGCA CTGACAAACA TCGCTGTGCT	300
AAAACATAAC TTGAACATCC TGATTAAACG CTCCAACCTCT ACCGCTGCTA CCAATGAGGT	360
TCCTGAGGTC GAG	373

## (2) INFORMATION FOR SEQ ID NO:118:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

GAATTCGGCC AAAGAGGCCT ACTTAACCAG AATGACAGTC TTTCCCTAT CTTCTTCTT	60
TATTCTTATC TTCTATCTTT CCCTCCCAA CTCTTTCCCC GACATAACAG AAAACATGAA	120
GGAATTAAAG GAGGCCAGGC CGCGCAAAGA TAACAGGCGT CCAGATCTGG AAATCTATAA	180
GCCTGGCCTT TCTCGGCTAA GGAACAAGCC CAAAATCAAG GAACCCCTG GGAGTGAGGA	240
ATTCAAAGAT GAAATTGTTA ATGACCGAGA TTGCTCTGCT GTTGAAAATG GTACACAGCC	300
CGTCGAG	307

## (2) INFORMATION FOR SEQ ID NO:119:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

GGAGCTGCAC ATGGTACTTT TGGAGAGCCT GGTGGAAATC ATTTTGGTTG CTGTTTCAGCA	60
TGTGGATTAT AGTCTTCGAT GTGAGCAGGA TCCAGAGAAG AAAGCTTTTA TCAGACAGAA	120
TGCATCCTTT TTATATGAAA CAGTCCTCCC TGTGGTGGAG AAAAGGTTTG AAGAAGGTGT	180
GGGGAAACCT GCCAAGCAAC TCCAAGATCT GAGGAATGCA TCTAGACTTA TTCGTGTGAA	240
TCCTGAAGTC GAG	253

## (2) INFORMATION FOR SEQ ID NO:120:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

GAATTCGGCC AAAGAGGCCT ACACATATTG GAAAAATGAT CTTTTTGGAG CACTGTTCTG	60
CTGCTTAGAC CCAGTACTCA CTATTGCTGC TAGTCTCAGT TTCAAAGATC CCATTTGTCA	120
TTCCACTGGG AAAAGAAAAG ATTGCAGATG CAAGAAGAAA GGAATTGGCA AAGGATACTA	180
GAAGTGATCA CTTAACAGTT GTGAATGCGT TTGAGGGCTG GGAAGAGGCT AGGCGACGTG	240
GTTTCAGATA CGAAAAGGAC TATTGCTGGG AATATTTTCT GTCTTCAAAC ACACTGCAGA	300
TGCTGCATAA CATGAAAGGA CAGTTTGCTG AGCATCTTCT TGGAGCTGGA TTTGTAAGCA	360
GTAAGAAATCC TAAAGATCCA GAATCTAATA TAAATTCAGA TAATGAGAAG ATAATTAAAG	420
CTGTCGAG	428

## (2) INFORMATION FOR SEQ ID NO:121:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GAATTCGGCC AAAGAGGCCT ACAAGACGTC ATTTCACAAA GTGCGCCATT CTGAGGATAT	60
GCAGTTTGCC TTCTCTTATT TTTATTATCT CATGAGTGCA GTGCAGCCAC TGAATATATC	120
TCAAGTCTTT GATGAAGTTG ATACAGATCA ATCTGGTGTC TTGTCTGACA GAGAAATCCG	180
AACACTGGCT ACCAGAATTC ACGAACTGCC GTTAAGTTTG CAGGATTGA CAGGTCTGGA	240
ACACATGCTA ATAAATTGCT CAAAAATGCT TCCTGCTGAT ATCACGCAGC TAAATAATAT	300
TCCACCAACT CAGGAATCCT ACTATGATCC CAACCTGCCA CCGGTCCTA AAAGTCTAGT	360
AACAACTGT AAACCAGTAA CTGACAAAAT CCACAAAGCA TATAAGGACA AAAACAAATA	420
TAGGTTTGAA ATCATGGGAG AAGAAGAAAT CGCTTTTAAA ATGATTTCGTA CCAACGTTTC	480
TCATGTGGTT GGCCAGTTGG ATGACATAAG AAAAAACCCT GTCGAG	526

## (2) INFORMATION FOR SEQ ID NO:122:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GGGTGGCAAT ATGGA	CTTCC	TCTTTCTGC	CANCCCANAC	CCATACATCG	GGATTCTAT	60
AATACCTTCG TTGGTCTCCC	TAACATGTAG	GTGGNGGNGG	GGAGATATAC	AATAGAACAG		120
ATACCAGACA AGACATAATG	GGCTAAACAA	GACTACACCA	ATTACACTGC	CTCATTGATG		180
GTGGNACATA ACGAGCTAAT	ACTGTAGCCC	TAGACTTGAT	AGCCATCATC	ATATCGAAGT		240
TTC	ACTACCC	TTTTTCCATT	TGCCATCTAT	TGAAGTAATA	ATAGGCGCAT	300
TTCTTTT	TTT	TTTCTC	TCTCCCCCGT	TGTTGTCGAG		340

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

GAATTCGGCC AAAGAGGCCT	ACGTCCTTTT	AAATCTTAAT	GAAATATCAT	GGAATATTGT	60
ATGGTCTTCA TATCGTTCTA	TATAATGCAA	ATGGTGAAC	GCTCTGTTCT	TTGCTTTCT	120
GAAAGCATCC ATCCGATCAG	TAGCTTTCCC	AATAGAAAAA	CCTGCAGCTC	CTTTTCCGTT	180
CCCCACAGCC ACCAAGACAC	GGATCGATTT	CTTTCTTCCC	TCTTTCGAG	TCATAGTGAA	240
AACGTTTCTT ACCTCAAGTA	TCCTGGTATC	AAAATCCTCA	TATGTTTCTC	CACAGTCGAG	300

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GAATTCGGCC AAAGAGGCCT	ACCAGCTTTG	AGGTTGACCT	GTTTCTCTTT	GTCTGCCTTC	60
CCAAAACACC AGCCCCAGG	AAGACATTAA	GCAGCCTTAA	GCTTAAATTC	CTACTCCCTC	120
TTCCAAATTT GGCTCACTTG	CCTTAGATCC	AAGGCAGGGA	AAGGAAAAGA	AGGGGGGTCT	180
CTGGCTTTAT TACTCCCTA	AGTCTTTACT	CTGACTTCCC	CAAACCCAGA	AAGATTTTCT	240
CCACACTGTT CATTTGAAAG	AGGAGTATTT	TGTCCCATTT	TCCCCTTCCT	CATTATCAAA	300
CAGCCCCAGT CTTCTTGTC	TCTGCTAAGA	AAGTAGAGGC	ATGATGATCT	GCCTCTCAAC	360
TGCCCTAGTC	GAG				373

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 644 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

GAATTCGGCC	AAAGAGGCCT	ACGCAGATAC	GGGCTTACAG	ATACTTTTTA	CACTCTTACA	60
AAATGTTGCA	CAAGAAGAAG	CTGCAGCTCA	GAGTTTTTAT	CAAACCTTAT	TTTGTGATAT	120
TCTCCAGCAT	ATCTTTTCTG	TTGTGACAGA	CACTTCACAT	ACTGCTGGTT	TAACAATGCA	180
TGCATCAATT	CTTGCAATATA	TGTTTAATTT	GGTTGAAGAA	GGAAAAATAA	GTACATCATT	240
AAATCCTGGA	AATCCAGTTA	ACAACCAAAT	CTTCTTCAG	AAATATGTGG	CTAATCTCCT	300
TAAGTCGGCC	TTCCCTCACC	TACAAGATGC	TCAAGTAAAG	CTCTTTGTGA	CAGGGCTTTT	360
CAGCTTAAAT	CAAGATATTC	CTGCTTTCAA	GGAACATTTA	AGAGATTTC	TAGTTCAAAT	420
AAAGGAATTT	GCAGGTGAAG	ACACTTCTGA	TTGTTTTTGT	GAAGAGAGAG	AAATAGCCCT	480
ACGGCAGGCT	GATGAAGAGA	AACATAAACG	TCAAAATGCT	GTCCCTGGCA	TC'TTAAATCC	540
ACATGAGATT	CCAGAAGAAA	TGTGTGATTA	AAATCCAAAT	TCATGCTGTT	TTTTTCTCT	600
GCAACTCGTT	AGCAGAGGAA	AACAGCATGT	GGTATTTTGT	CGAG		644

## (2) INFORMATION FOR SEQ ID NO:126:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

GAATTCGGCC	AAAGAGGCCT	ACGTTATACT	ATTAGATCCT	TTCATTATCA	ATCCCTTTTA	60
AAGGCAAGGA	AACAGGTTCA	GCAAGATCAG	CTGACTTCTC	TGTGTAAGTG	GGACCTGAGA	120
TTTGAAAGTT	GAGAGCAGCA	TGTTTTGCCC	ACTGAAACTC	ATCCTGCTGC	CAGTGTTACT	180
GGATTATTCC	TTGGGCCTGA	ATGACTTGAA	TGTTTCCCCG	CCTGAGCTAA	CAGTCCATGT	240
GGGTGATTCA	GCTCTGATGG	GATGTGTTTT	CCAGAGCACA	GAAGACAAAT	GTATATTCAA	300
GATAGACTGG	ACTCTGTAC	CAGGAGAGCA	CGCCAAGGAC	GAATATGTGC	TATACTATTA	360
CTCCAATCTC	AGTGTGCCTA	TTGGGCGCTT	CCAGAACCGC	GTACACTTGA	TGGGGGACAA	420
CTTATGCAAT	GATGGCTCTC	TCCTGCTCCA	AGATGTGCAA	GATGTCGAG		469

## (2) INFORMATION FOR SEQ ID NO:127:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GAATTCGGCC	AAAGAGGCCT	AGAGGGGACT	CGCCGCCATC	TCAGGTCTCT	TGGCTTTGCC	60
AGGGCCCACC	GGAGAAAAC	TGACACCCGT	TTCTGTAATC	CTTATGGGAG	ACCAACCTTG	120
TGCCTCCGGG	AGATCCACTC	TCCACCTGG	AAACGCACCG	GAAGCCAAGC	CTCCAAAAAA	180
GCGCTGCCTC	CTCGCTCCGC	GTTGGGATTA	TCCGGAAGGA	ACTCCCAACG	GAGGTAGTAC	240
CACTCTACCC	TCCGCACCTC	CTCCTGCATC	AGCCGGCCTG	AAGTCGCACC	CTCCTCCTCC	300
GGAGAAGTAG	AGAAATAAAT	TTCTCCCACC	CTAAACCACT	CTTTGAGTGA	TGTCAGTATG	360
ACTCCATTTT	CCTGGTGCAT	TCATATAATA	GTTACCTGG	TGAAAACAAT	GAAGATTATT	420
TACAATGCTA	CCCCG					435

## (2) INFORMATION FOR SEQ ID NO:128:

## (i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

```
GAATTCGGCC AAAGAGGCCT AACCAAGCAG AAGCTGTACC ACAAGAAGAT CTCCGGACT    60
GCCATGCTGT TCCAGTTTGT GAACGTGCTG CTCCAGGTCC TGGTCCACAA GTCCCATGAT    120
CTTCTGCAGG AGGAGATTGG CATCGCCATC TACAACATGG CCTCAGTCGA G            171
```

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

```
GAATTCGGCC AAAGAGGCCT AGTCATGACT CCCCTGATTI GGCTCCTAAT GTCACTTATT    60
CCCTGCCCAG AACCAAAAGT GGTAAGCCC CAGAAAGAGC CTCTAGCAAG ACTTCTCCAC    120
ATTGGAAGGA GTCAGGAGCC TCCCATTGT CATTCCTAAA GAACAGCAAA TATGAGTATG    180
ACCCTGACAT CTCTCTCCA CGAAAAAGC AAGCAAAATC CCATTTTGA GACAAGAAGC    240
AGCTTGATTG CAAAGGTGAC TGCCAGAAAG CAACTGATTC AGACCTTCT TCTCCACGGC    300
ATAAACAAAG TCCAGGGCAC CAGGATTCTG ATTCAGATCT GTCACCTCCA CGGAATAGAC    360
CTAGACACCG GG                                                    372
```

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

```
GAATTCGGCC NAAGAGGCCT AGGGTGGGAC AAGAGAGTGA GACTAGAATA TAAATATCCG    60
TAAACAGCAT CTGAGCATTG GTCTTTAACA GGGAGGAGGA ACCACTGGTG TATATTAATT    120
TAGGACACAG GATCATTATA GGGGTNGGGC CAGCTGGTGT TAATGGCATG CAGGCATATG    180
TGATGCCAAC CATGAGGGCT GGAAGAACCA GAAGCCAAAG AAGAATATGA CCGCATCTAT    240
TCTAAAGCTA CTGTGGTGGT TTCTCATGCT TCAGAGTCTC GTAAGTCTCC TGGTTCCTGG    300
TGCTCAGGCC CGTGTAACA CCATCTGATT TCTCATAGCT GGTATAGCT GCCTTCGCA    360
CTTGATCTT CAGTCGAG                                                    378
```

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

```
GAATTCGGCC AAAGAGGCCT AGGTGCCGCG GTCCTGTCTT GCTGTGCCTG CGGCAGGGGC      60
TCGGAACCAA TTCATTCCCTG CACGGCCTGG GGCAGGAGCC CTCGAGGGA GCTCGGTCAC      120
TGTGTTGCAG GTCCTCGCCT AGAGACCTGC GAGATGGAGA AAGAGAGCAC GAGGCGGCAC      180
AAAGGAAAGC CCCAGGAGCA GAGTCTTGCC CATCTCTCCC TCTGAGCATC TCGGACATTG      240
GGACTGGATG TCTTTCGTCA CTGGAAAACC TCAGACTGCC GACGCTGCCG GAAGAGTCAT      300
CCCCTCGAGA GCTCGAGGAC TCGAGCGGAG ACCAGGGCCG GTGCGGTCCC ACACACCAGG      360
GATCCGAGGA TCCTTCGATG CTCTCGCAGG CCCAGTCCGC TACCGAGGGT CGAG          414
```

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

```
AAGCGTGCTC GTGCCCCGTAT TNCCNAGGGG NTCAGTCTGT NNCGCCCANA GNCCAAGNCC      60
AAGCCCCAGN CCNAGNCCAA GGATCCANNC CAAGGCCCCAG GCTGCAGCCC CAGCTTCAGT      120
TCCAGCTCAG GCTCCACAC GTACCCAGGC CCCACAAAG GCTTCAGAGN AGATATCTCT      180
CCCAACATGA GGACAGAAGG ACTGGTGCGA CCCCCACCC CCGCCCCTGG GCTACCATCT      240
GCATGGGGCT GGGTCCTCCT GTGCTATTG TACAAATAAA CCTGAGGCAG TCGAG          295
```

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

```
ATGGACTTCC TCTTTTCTGC CANCCACAC CCATACATCG GGAGCCTATA ATACCCTTCG      60
TTGNTCTCCC TAACATGTAG GTGGCGGAGG GGAGATATAC AATAGAACAG ATACCAGACA      120
AGACATAATG GGCNNAACAA GACNACACCA ATTACNCTNC CTCATTGATG GTGGNACATA      180
ACGAGCTAAT ACTGTANCCC TAGACNTGAT AGCCATCATC ATATCGAAGT TTCCTACCC      240
TTTTTCCATT TGCCATCTAT TGAAGTAATA ATAGGCGCAT GCAACTTCTT TTCTTTTTTT      300
TTCTTTTCTC TCTCCCCCGN TGTGTCTCA CCATATCCGC AATGACGTCG AG          352
```

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GAATTCGGCC	AAAGAGGCCT	ACGTTATCCG	CGATGCGTTT	CCTGGCAGCT	ACATTCCTGC	60
TCCTGGCGCT	CAGCACCGCT	GCCCAGGCCG	AACCGGTGCA	GTTCAAGGAC	TGCGGTTCTG	120
TGGATGGAGT	TATAAAGGAA	GTGAATGTGA	GCCCATGCCC	CACCCAACCC	TGCCAGCTGA	180
GCAAAGGACA	GTCTTACAGC	GTCAATGTCA	CCTTCACCAG	CAATATTCAG	TCTAAAAGCA	240
GCAAGGCCGT	GGTGCATGGC	ATCCTGATGG	GCGTCCAGT	TCCCTTTCCT	ATTCTTGAGC	300
CTGATGGTTG	TAAGAGTGGA	ATTAAGTCC	CTATCCAAAA	AGACGTCGAG		350

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

GAATTCGGCC	AAAGAGGCCT	ATTGAATTCT	AGACCTGCGT	CGACCTCCCT	TCCAGCCCCC	60
AGAAAGCTCG	GTCACCTGAG	TGTTTCTAG	AATCCTGGGG	TGCTCCCGGG	CCGCTCTCAG	120
AGAAGTGGCA	GGTTTCACGT	TCAGCCGTGT	GGCGGATCGT	GTGGCTTCCA	AAGCCTTTTA	180
CAGCCCCCGC	CCCCCATCCC	GTGGTCTGTC	TGCAGGAACT	CTCCCGTCTG	TGAGAAGCCT	240
CTTTCCGAGT	CGAG					254

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

GAATTCGGCC	AAAGAGGCCT	ACTAGAGGGG	TCAGTGGCCC	CGCACGGTGG	GGTGGCCGCT	60
CAGGGCCTAG	GGAGCAGGTG	GGAGGGGCTT	GGAGGGCAGA	ACAGAGGGCC	TGGGGGCTGC	120
TCTGCTGGCC	ACCACTGCTT	TCTGGTTGAA	CCAGATAAGT	AGCTGGTGGT	GACGGCTGTG	180
GGCCCTGAGT	CGGGGGAGAA	GAGGCAGAGG	GAGCAGTGGG	CTGGGCTAGT	GGGGACATGA	240
GTGGGTGGTG	ATCATGCCTG	TGTCGGGGGA	GCTGAGGCAG	AGAGTGGGGC	AGCGAGCATC	300
CCCTGAGGGC	AGGAGGAGAG	GGGTGGGGAC	AGGGAAGGGT	CGGGGGTGGT	CCCAGCCCTG	360
AAGACAGGAG	TGGCGAGGGC	AGGTGTGCTC	TAGGTGCTTG	TCGAGGTGGA	CAACATGGGT	420
CGAG						424

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

GAATTCGGCC	AAAGAGGCCT	AATGGCGTCC	AGGTCTAAGC	GGCGTGCCGT	GGAAAGTGGG	60
GTTCCGCAGC	CGCCGGATCC	CCCAGTCCAG	CGCGACGAGG	AAGAGGAAAA	AGAAGTCGAA	120
AATGAGGATG	AAGACGATGA	TGACAGTGAC	AAGGAAAAGG	ATGAAGAGGA	CGAGGTCATT	180
GACGAGGAAG	TGAATATTGA	ATTTGAAGCT	TATTCCTAT	CAGATAATGA	TTATGACGGA	240
ATTAAGAAAT	TACTGCAGCA	GCTTTTTCTA	AAGGCTCCTG	TGAACACTGC	AGAACTAACA	300
GATCTCTTAA	TTCAACAGAA	CCATATTGGG	AGTGTGATTA	AGCAAACGGA	TGTTTCAGAA	360
GACAGCAATG	ATGATATGGA	TGAAGATGAG	GTTTTTGTT	TCATAAGCCT	TTTAAATTTA	420
ACTGAAAGAA	AGGGTACCCA	GTGTGTTGAA	CAAATTCAG	AGTTGGTTCT	ACGCTTCTGT	480
GAGAAGAACT	GTGAAAAGAG	CATGGTTGAA	CAGCTGGACA	AGTTTTTAAA	TGACACCACC	540
AAGCCTGTGG	GCCTTCTCCT	AAGTGAAAGA	TTCATTAAATG	TCCCTCCACA	GATCGCTCTG	600
CCCATGTACC	AGCAGCTTCA	GAAAGAACTG	TCGGGGGCAC	ACAGAACCAA	TAAGCCATGT	660
GGAAGTGCT	ACTTTTACCT	TCTGATTAGT	AAGACATTTG	TCGAG		705

## (2) INFORMATION FOR SEQ ID NO:138:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

GAATTCGGCC	AAAGAGGCCT	ACCCAGCTCA	GAATCTTGCT	GCTCGGCCCC	CAGGAGAGCA	60
ACAACACAAC	GGGAACGATG	TGGAAGGTGT	CAGCTCTGCT	CTTCGTTTTG	GGAAGCGCGT	120
CGCTCTGGGT	CCTGGCAGAA	GGAGCCAGCA	CAGGCCAGCC	AGAAGATGAC	ACTGAGACTA	180
CAGGTTTGGA	AGGCGGCGTT	GCCATGCCAG	GTGCCGAAGA	TGATGTGGTG	ACTCCAGGAA	240
CCAGCGAAGA	CCGCTATAAG	TCTGGCTTGA	CAACTCTGGT	GGCAACAAGT	GTCAACAGTG	300
TAACAGGCAT	TCGCATCGAG	GATCTGCCAA	CTTCAGAAAG	CCCAGTCGAG		350

## (2) INFORMATION FOR SEQ ID NO:139:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GAATTCGGCC	AAAGAGGCCT	AGTGGACAGG	AAGTAGAATT	TATTGGTGAG	TATTAAGAGG	60
GGGGCAGCAC	ATTGGAAGCC	CTCATGAGTG	CAGGGCCCGT	CACTTGTCCA	GAGGGCCACG	120
ACTGGGGATG	TACTTGACCC	CACAGCCATC	TGGGATGAGC	CGCTTTTCAG	CCACCATGTC	180
TTCAAATTCA	TCAGCATTGA	ACTTGGTGAA	GCCCCACTTC	TTGAGATGT	GGATCTTCTG	240
GCGGCCAGGA	AAC TTGAACT	TGGCCCTGCG	CAGGGCCTCA	ATCACATGCT	CCTTGTTCTG	300
CAGCTTGGTG	CGGATGGACA	TGATAACTTG	GCCAATGTGA	ACCCTGGCCA	CAGTGCCCTG	360
GGGCTTTCCA	AAGGCACCTC	GCATGCCTGT	TTGGAGCCTG	TCAGCCCCAG	CACAGGACAA	420
CATCTTGTG	ATGCGGATGA	CGTGGTCGAG				450

## (2) INFORMATION FOR SEQ ID NO:140:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 585 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

```
GAATTCGGCC AAAGAGGCCT ATGAAGATCA GCTATTAGAA GAGAAAGATC AGTTAAGTCC      60
TTTGGACCTG ATCAGCTTGA TACAAGAACT ACTGATTTCA ACTTCTTTGG CTTAATTCTC      120
TCGGAAACGA TGAATATATAC AAGTTATATC TTGGCTTTTC AGCTCTGCAT CGTTTTGGGT      180
TCTCTTGGCT GTTACTGCCA GGACCCATAT GTAAAAGAAG CAGAAAACCT TAAGAAATAT      240
TTTAATGCAG GTCATTGAGA TGTAGCGGAT AATGGAAGTC TTTTCTTAGG CATTTTGAAG      300
AATTGGAAAG AGGAGAGTGA CAGAAAAATA ATGCAGAGCC AAATTGTCTC CTTTACTTTC      360
AAACTTTTTA AAAACTTTAA AGATGACCAG AGCATCCAAA AGAGTGTGGA GACCATCAAG      420
GAAGACATGA ATGTCAAGTT TTTCAATAGC AACAAAAAGA AACGAGATGA CTTCGAAAAG      480
CTGACTAATT ATTCGGTAAC TGACTTGAAT GTCCAACGCA AAGCAATACA TGAAGTCATC      540
CAAGTGNTGG CTGAAGTGTG GCCAGCAGCT AAAACAGGGG TCGAG                        585
```

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 471 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

```
GAATTCGGCC AAAGAGGCCT ATTGGAGTTT GAGTATAGTA AATTATGATC CTTAAATATT      60
TGAGAGTCAG GATGAAGCAG ATCTGCTGTA GACTTTTCAG ATGAAATTGT TCATTCTCGT      120
AACCTCCATA TTTTCAGGAT TTTTGAAGCT GTTGACCTTT TCATGTTGAT TATTTTAAAT      180
TGTGTGAAAT AGTATAAAAA TCATTGGTGT TCATTATTTG CTTGTCCTGA GCTCAGATCA      240
AAATGTTTGA AGAAAGGAAC TTTATTTTTC CAAGTTACGT ACAGTTTTTA TGCTTGAGAT      300
ATTTCAACAT GTTATGTATA TTGGAAGTTC TACAGCTTGA TGCCTCCTGC TTTTATAGCA      360
GTTTATGGGG AGTCACTTGA AAGAGCGTGT GTACATGTAT TTTTCTCTN GGCAAACATT      420
GAATGCAAAC GTGTATTTT TTAATATAAA TATATAACTT CCTGCGTCCA G                        471
```

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 477 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

```
GAATTCGGCC AAAGAGGCCT ATGTTTGGCA ACTGGGGTGA AGGGATTGCC CTCCCCCTGC      60
TGGGATCCCC CCAGCCCTC CGGTCTGGCA GGAAGGGGGC AGCCTGCAAC CCCCAAGGGC      120
AGGTGTGGGG CTGCCAGATG CTCCAGGCAG GGGGCCAGAA GGGGCTCACA AAGGCTTGCC      180
CTCCAGGGAG ATGACGGCAC TGCCCCCAG CTTCTCTGCC AGGGTGACGC GGTCTTGAGC      240
CTCCTCGTAG CAGTTTGCTT GCAATTCATG CTTGATCCCT GTCAGCTTCT TCTTGATGGC      300
GTCCTTGGAG CTGGCATAAA TCATTTTGCT CTTAAGGGGS GCAGACTCGG GGGCCCAGAA      360
GATAAACACC AGATCCTCCT TCTTGCTCTC CYTGGTCTCA TAGGTTGCAT CATAGAGGGC      420
```

ATAGCGGCAG TCCTTATCTG GCAGCATCTT GACAAAGGTG GCGTAGGGAT CGTCGAG

477

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

GAATTCGGCC CAAAGAGGCC YMAAGATCA GCTATTAGAA GAGAAAGATC AGTTAAGTCC	60
TTTGGACTTG ATCAGCTTGA TACAAGAACT ACTGATTTC ACTTCTTTGG CTTAATTCTC	120
TCGGAACCGA TGAAATATAC AAGTTATATC TTGGCTTTTC AGCTCTGCAT CGTTTGGGT	180
TCTCTTGGCT GTTACTGCCA GGACCCATAT GTAAAAGAAG CAGAAAACCT TAAGAAATAT	240
TTAATGCAG GTCAATCAGA TGTAGCGGAT AATGGAACTC TTTTCTTAGG CATTTTGAAG	300
AATTGGAAG AGGAGAGTGA CAGAAAAATA ATGCAGAGCC AAATTGTCTC CTTTACTTC	360
AAACTTTTAA AAAACTTTAA AGATGACCAG AGCATCCAAA AGAGTGTCTGA G	411

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

GAATCGGCCC AAAGAGGCCT ACTGAAGATC AGCTATTAGA AGAGAAAGAT CAGTTAAGTC	60
CTTTGGACCT GATCAGCTTG ATACAAGAAC TACTGATTTT AACTTCTTTG GCTTAATTCT	120
CTCGGAAACG ATGAAATATA CAAGTTATAT CTTGGCTTTT CAGCTCTGCA TCGTTTGGG	180
TTCTCTTGGC TGTTACTGCC AGGACCCATA TGTAAGAGAA GCAGAAAACC TTAAGAAATA	240
TTTAATGCA GGTCAATCAG ATGTAGCGGA TAATGGAACCT CTTTCTTAG GCATTTTGAA	300
GAATTGGAAA GAGGAGAGTG ACAGAAAAAT AATGCAGAGC CAAATTGTCT CCTTTACTT	360
CAAACTTTT AAAAATTTA AAGATGACCA GAGCATCCAA AAGAGTGTGG AGACCATCAA	420
GGTCGAG	427

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 598 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

GAATTCGGCC AAAGAGGCCT AGAGAAGATA AACTGGACA CTGGGGAGAC ACAACTTCAT	60
GCTGCGTGGG ATCTCCAGC TACCTGCAGT GGCCACCATG TCTTGGGTCC TGCTGCCTGT	120
ACTTTGGCTC ATTGTCAAA CTCAAGCAAT AGCCATAAAG CAAACACCTG AATTAACGCT	180
CCATGAAATA GTTTGTCCTA AAAAATTCA CATTTTACAC AAAAGAGAGA TCAAGAACAA	240

CCAGACAGAA AAGCATGGCA AAGAGGAAAG GTATGAACCT GAAGTTCAAT ATCAGATGAT	300
CTTAAATGGA GAAGAAATCA TTCTCTCCCT ACAAAAAACC AAGCACCTCC TGGGGCCAGA	360
CTACACTGAA ACATTGTACT CACCCAGAGG AGAGGAAATT ACCACGAAAC CTGAGAACAT	420
GGAACTGT TACTATAAAG GAAACATCCT AAATGAAAAG AATTCTGTG CCAGCATCAG	480
TACTTGTGNC GGGTTGAGAG GATACTTCAC ACATCATCAC CAAAGATACC AGATAAAACC	540
TCTGAAAAGC ACAGACGAGA AAGAACATGC CGTCTTTACA TCTAACCAGG AGGTCGAG	598

## (2) INFORMATION FOR SEQ ID NO:146:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GAATTCGGCC AAAGAGGCCT AGAGCTAAGG CGAAGACCAA GACACGTGAC ATTCATGCTT	60
TGGTGTGGGG TCCAAAGCAC TCTTATTAA CATAGATTCC AAACCTTTTA CACCCATGGG	120
GTCATATATA CTCTTTATTT TACCCTTCAT TATTTTAAAA ATCACAACAT CACCCATTGC	180
CCCCGTGTCC AAAGGAATCG CTTGTAATAA ATCAGCAGGT CTAGAATTCA ATCGGGAG	238

## (2) INFORMATION FOR SEQ ID NO:147:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

GAATTCGGCC AAAGAGGCCT AGAGCTAAGG CGAAGACCAA GACACGTGAC ATTCATGCTT	60
TGGTGTGGGG TCCAAAGCAC TCTTATTAA CATAGATTCC AAACCTTTTA CACCCATGGG	120
GTCATATATA CTCTTTATTT TACCCTTCAT TATTTTAAAA ATCACAACAT CACCCATTGC	180
CCCCGTGTCC AAAGGATTCC CTTGTAATAA ATCAGCAGGT CTAGAATTCA ATCGGGAGGT	240
TCTCCCTATA GTGAGTCGTA TTAATTCAG AGGAGTATT AGAAGAGAAG CTGAAGCTGT	300
CGAG	304

## (2) INFORMATION FOR SEQ ID NO:148:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

GAATTCGGCC AAAGAGGCCT ACGACAGTTG GTGTAAAGGA AAACCTCTGA GCTCCGTCAG	60
TTCACCTGGT ACATTGGAAT TAAAGTGCTT GGATGTTTTT CCCCCACTTT AAAAAAATT	120
TTGAGGTTTT TTTTTTTTTT TGCTTTTAA AAACATCGTA ACATTAACAC ATGGCCGTTT	180
ACCGTCCCCC AGCGATGGGA GCTGGCCTGG GGCCAGGGT CCTCCAGGAT CTCACTCAT	240

TCACAGTAAC GGTCTGACC AGTCCTCCAG GTCGCACGTG GATGCGACAG GGGTGGGGAG	300
GGAGGAGGAA GTGACTGTCC CACCTCTGCA GGACCATGGG AGTGGGCAAG GTCTTCTCCG	360
GGGCGCACCC CTGAACCCAG GGGTGCTGCA GGACNTG	397

## (2) INFORMATION FOR SEQ ID NO:149:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 592 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

GAATTCGGCC AAAGAGGCCT ATAAGAATTT AAGATGCATT TTTGCATTG CTATATTTCT	60
TTAAATTCTA GATAGTTATT TTCAAGTGTT GGTAAACATA AATCTTAGGC TTAGGAACCA	120
TTGGATTAGT AACAGCATTG TGCTAATCAA AACTTTAAAA AAATGAGTTC AAAATTGTGA	180
TAATGTAATT TTATAGATT TCTTTTATCC TCAACCTGCA GAAGCCGAA AGTGAGGCAC	240
ATAGCCCCAC ATAGGCAGAA ATTAAGCCT AGGCAATAAC TTAGTGAAAA TGGAAATTTTC	300
AGAACATTCC ACTTCTTGT TAGTACAATT TTATGGCCAT GGTGCTAGCT AATGGAAATG	360
GCTAGTATAC TATTATAGG CCAGCAATAT TTTGGTGAAT TTAAGCGAAA CTATGCTCAG	420
TATCATTGAA ATGGGGGTGG GGTGGGCTTG AGACATGAAA TCAATCATAC AAAGTCAAAA	480
ACTATTTTAA CCCAGGAATA AGTTAAATTC CTGTCACCCA GTCGAGGTTC TCCCTATAGT	540
GAGTCGTATT AATTTCAGAG GAGTATTTAG AAGAGAAGCT GAAGCTGTCT AG	592

## (2) INFORMATION FOR SEQ ID NO:150:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

GAATTCGGCC AAAGAGGCCT AGATGATGAT ATGTTTAAACC ACCAAGTTCC TTATTTGTGG	60
CTGATTTACT GCCTTTGTCA TCCTCTCAA TCAAGTATTA AAGAAACAGT GGAGGCATAT	120
GAGGCAGCAT TAGGGGTGGC TATGAGATGT GATATAGTAC AGAAGATATG GATGGATTAT	180
CTTGTCTTTG CAAATAATAG AGCTGCTGGA TCCAGAAACA AAGTTCAAGA ATTCAAATTT	240
TTTACTGATT TAGTGAATAG ATGTTTGTT ACAGNCCCTG CCCGATACCC CATTCTTTT	300
AGCAGNGCTG ATTACTGGTC CAACTATGAA TTTCATAATA GGGTCGAG	348

## (2) INFORMATION FOR SEQ ID NO:151:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

GAATTCGGCC AAAGAGGCCT ACAGAATTGA GASTTTGTTT TTACACACAA GTTTAATGCC	60
---	----



```

ACCTTCCTCT GTCTGCCATG GACCAACAAG CAATATATGC TGAGTTAAAC TTACCCACAG      120
ACTCAGGCCC AGAAAGTTCT TCACCTTCAT CTCTTCCTCG GGATGTCTGT CAGGGTTCAC      180
CTTGGCATCA ATTTGCCCTG AAACCTAGCT GTGCTGGGAT TATTCTCCTT GTCTTGGTTG      240
TTACTGGGTT GAGTGTTTCA GTGACATCCT TAATACAGAA ATCATCAATA GAAAAATGCA      300
GTGTGGACAT TCAACAGAGC AGGAATAAAA CAACAGAGAG ACCGGGTCTC TTAAACTGCC      360
CAATATATTG GCAGCAACTC CGAGTCGAGG TTCTCCCTAT AGTGAGTCGT ATTAATTTC      420
GAGGAGTATT TAGAAGAGAA GCTGAAGCTG TCGAG                                455

```

## (2) INFORMATION FOR SEQ ID NO:152:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

```

GAATTCGGCC AAAGAGGCCT AAAAATCTCT TATTAAAGGT AGAACCTCTG CTAGCCAGAC      60
AACTATATTA TTTTGCTCAA CAAAACAGTG GACATTTCTT GAGGGGCTAC GATTACCAG      120
AACACATCAG CAATCCAGAA GATTACCACA GATCTATCCG CCATTCCTCT ATCAAGAAT      180
GAAAAATGTC AAGATGAGTG GTTTTCTTTT TCCTTTT TTTT TTTTGATACG      240
GGGATACGGG GTCTTGCTCT GTCTCCAGG CTGGAGTGCA GTGACACAAT CTCAGCTCAC      300
TGTGACCTCC GCCTCCTGGG TTCAAGAGAC TCTCTGCCT CAGTCGAG                    348

```

## (2) INFORMATION FOR SEQ ID NO:153:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

```

GAATTCGGCC AAAGAGGCCT ACCTTAAAGC CGTATACTTA TGAATTTAAA GTGGAAAATT      60
TTTTTGGTGG CCCTGGCCCC CTTGCCAGAT TCCAGCTGGC CGTCAGTGCT CGCGTGTCTC      120
TCTGAAGAGG CTCTGCGGTT CTGGTCCCTG TGCCTGAGCT CCAGGTGCCG CCAGACATTA      180
TACAACGTGA AGGCTGAGAT CTTTCCCCCT TCGGGAATGG AGTATTGCAG AACAGGCTCC      240
CTCTGCTCCC TGGAGGTTTT GATCACGAGG CTCTCAGACC TCTTGGAGGT GGATAAAGAT      300
GAAGCACTGA CTGAATCTGA TGAGCATTTT TCGACAAAGC TTATGTATGA AGTTGTCGAG      360

```

## (2) INFORMATION FOR SEQ ID NO:154:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

```

GAATTCGGCC AAAGAGGCCT ACTCATCTTG GGTCCCAGCC AGGCCCCCCC AAAACCAAAG      60

```

CCCCTTCAAG	TCCTGGGGTC	CCAGCCTGTG	CCCCCAGCTT	CCTGCCCACC	CAGCCCCGAG	120
CATTCTCACA	CAGAGAAAGA	ACAAGCAAGG	GCTCCAGGGG	GACAGGATGG	GGCAGGGCAT	180
ACAGTGGGGG	GTGGGGGGGC	AGCTGGGAGG	AGGGAGGGAC	AAAACAAAAC	ATTTTCCTTT	240
GGGTTTTTTT	TTTCTTTCTT	TTTTCTCCCC	TTTACTCTTT	GGGTGGTGTT	GCTTTTCCTT	300
TCCTTTTCCC	TTTGAGATTT	TTTGTTGTTT	GTTCCTTTT	TGTATTTTAC	TGATATCACC	360
AGGATAGTTT	ACTCTCCTTC	TAGCTTTCTG	CTTACCGCAC	ACTGGATAAC	ACACACATAC	420
ACACCCACAA	AAATGCTCAT	GAACCCAATC	CGGAGAAGGT	TCCAGCAGGT	CCCCCACCTT	480
CCCCCTCTCC	TCCTACTTCT	CCTCTTGACA	GCGAGGACAG	GAGGGGGACA	AGGGGACACC	540
TGGGCAGACC	CGCCGGCTCT	CCCCCACCC	CACCCGTCG	AG		582

## (2) INFORMATION FOR SEQ ID NO:155:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

GAATTCGGCC	AAAGAGGCCT	AGAAATAAAA	CATTCTACAC	CGTCTCCTAC	CAAATATTCA	60
CTATACCAA	GTAAAAGTTA	CAAGGTAAAC	AGGAAAGAAT	GGAATCATTT	CATTGTGAAA	120
TTGTTTCTGT	TCTAAGTGT	TTAAATGCTG	TTTTGTTATT	TTTATTTTTT	TTTTCAGTAT	180
TCTCCCGAAA	CACCACCTCG	ATGGACAGAA	GATCGGAATT	CTTTACTGAA	TATGATTTCG	240
CAACAAGTAG	AGGCCATGTC	GAG				263

## (2) INFORMATION FOR SEQ ID NO:156:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GAATTCGGCC	AAAGAGGCCT	AATTTCTCAG	CTCCAAGCAT	TAGGTAAACC	CACCAAGCAA	60
TCCTAGCCTG	TGATGGCGTT	TGACGTCAGC	TGCTTCTTTT	GGGTGGTGCT	GTTTCTGCC	120
GGCTGTAAAG	TCATCACCTC	CTGGGATCAG	ATGTGCATTG	AGAAAGAAGC	CAACAAAACA	180
TATAACTGTG	AAAATTTAGG	TCTCAGTGAA	ATCCCTGACA	CTCTACCAA	CACAACAGAA	240
TTTTTGGAAT	TCAGCTTTAA	TTTTTGCCT	ACAATCACA	ATAGAACCTT	CAGCAGACTC	300
ATGAATCTTA	CCTTTTGGGA	TTTAACTAGG	TGCCAGATTA	ACTGGATACA	TGAAGACACT	360
TTTCAAAGCC	ATCATCAATT	AAGCACACTT	GTGTTANCTG	GAAATCCCCT	GATATTCTATG	420
GCAGAAACAT	CGCTTAATGG	GCCCAAGTCA	CTGAAGCATC	TTTCTTAAT	CCANNCGGGA	480
ATATCCAATC	TCGAGTTTAT	TCCAGTGCAC	AATCTGGAAA	ACTTGAAAG	CTTGTATCTT	540
GGAAGCAACG	TCGAG					555

## (2) INFORMATION FOR SEQ ID NO:157:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

GAATTCGCCC AAAGAGGCCT AGATGATGAT ATGTTTAAACC ACCAAGTTCC TTATTTGTGG	60
CTGATTTACT GCCTTTGTCA TCCTCTTCAA TCAAGTATTA AAGAAACAGT GGAGGCATAT	120
GAGGCAGCAT TAGGGGTGGC TATGAGATGT GATATAGTAC AGAAGATATG GATGGATTAT	180
CTTGTCTTTG CAAATAATAG AGCTGCTGGA TCCAGAAACA AAGTTCAAGA ATTCAAATTT	240
TTTACTGATT TAGTGAATAG ATGTTTGTTT ACAGNCCCTG CCCGATACCC CATTCTTTT	300
AGCAGNGCTG ATTACTGGTC CAACTATGAA TTTATAATA GGGTCGAGGT TCTCCCTATA	360
GTGAGTCGTA TTAATTCAG AGGAGTATTT AGAAGAGAAG CTGAAGCTGT CGAG	414

## (2) INFORMATION FOR SEQ ID NO:158:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 590 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

GAATTCGGCC NAAGAGGCCT AAGCAGATGC TGATCTCATT ATGCTTGGCC TTGCCACACA	60
TGAACCGAAC TTTACCATT TTAGAGAAGA ATTCAAACCA AACAAGCCCA AACCATGTGG	120
TCTTTGTAAT CAGTTTGGAC ATGAGGTCAA AGATTGTGAA GGTTCGCCAA GAGAAAAGAA	180
GGGAAAGCAT GATGAACTTG CCGATAGTCT TCCTTGTGCA GAAGGAGAGT TTATCTTCCT	240
TCGGCTTAAT GTTCTTCGTG AGTATTGGA AAGAGAACTC ACAATGGCCA GCCTACCATT	300
CACATTTGAT GTTGAGAGGA GCATTGATGA CTGGGTTTTT ATGTGCTTCT TTGTGGGAAA	360
TGACTTCCTC CCTCATTGC CATCGTTAGA GATTAGGGAA AATGCAATTG ACCGTTTGGT	420
TAACATATAC AAAAATGTGG TACACAAAAC TGGGGGTTAC CTTACAGAAA GTGGTTATGT	480
CAATCTGCAA AGAGTACAGA TGATCATGTT AGCAGTTGGT GAAGTTGAGG ATAGCATTTT	540
TAAAAGAGA AAGGATGATG AGGACAGTTT TAGAAGACGA CAGGGTCGAG	590

## (2) INFORMATION FOR SEQ ID NO:159:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

GAATTCGGCC AAAGAGGCCT AGACGGGCCT CGGTCAGCAG CACGGGGTGC TCCTCGGGAG	60
CCACACGCAG CTCATTGTAG AAGGTGTGGT GCCAGATTTT CTCATGTGCG TCCAGTTGG	120
TGACGATGCC GTGCTCGATG GGGTACTTCA GGGTGAGGAT GCCTCTCTTG CTCTGGGCCT	180
CGTCGCCCAC ATAGGAATCC TTCTGACCCA TGCCCAACAT CAGGCCCTGG TGCTGGGGC	240
GCCCCACGAT GGAGGGGAAG ACGGCCCGGG GGCATCGTC CCCCAGGAAG CCGGCCTTGC	300
ACATGCCGGA GCCGTTGTG AG	322

## (2) INFORMATION FOR SEQ ID NO:160:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

```

GGGTTGACAA ATATGGACTT CCTCTTTTCT GCCNNCCCAA ACCCATACAT CGGGATTTCCT    60
ATAATACCTT CTTGGTCTC CCTAACATGT AGGTGGCGGA GGGGAGATAT ACAATAGANC    120
AAGATACCAG ACAAGACATA ATGGGCTAAA CAAGACTACA CCAATTACAC TGCCTCATTG    180
ATGGTGGTAC ATAACGAACT AATACTGTAG CCCTAGACTT GATAGCCATC ATCATATCGA    240
AGTTTCACTA CCCTTTTTC ATTTGCCATC TATTGAAGTA ATAATAGGCG CATGCAACTT    300
CTTTTCTTTT TTTTCTTTT CTCTCTCCCC CGTTGTTGTC TCACCATAG    349

```

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 688 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

```

GAATTCGGCC AAAGAGGCCT ACTATAAGAG AGATCCAGCT TGCCTCCTCT TGAGCAGTCA    60
GCAACAGGGT CCCGTCCTTG ACACCTCAGC CTCTACAGGA CTGAGAAGAA GTAAAACCGT    120
TTGCTGGGGC TGGCCTGACT CACCAGCTGC CATGCAGCAG CCCTTCAATT ACCCATATCC    180
CCAGATCTAC TGGGTGGACA GCAGTGCCAG CTCTCCCTGG GCCCCTCCAG GCACAGTTCT    240
TCCCTGTCCA ACCTCTGTGC CCAGAAGGCC TGGTCAAAGG AGGCCACCAC CACCACCGCC    300
ACCGCCACCA CTACCACCTC CGCGCCCGCC GCCACCACTG CCTCCACTAC CGCTGCCACC    360
CCTGAAGAAG AGAGGGAACC ACAGCACAGG CCTGTGTCTC CTTGTGATGT TTTTCATGGT    420
TCTGGTTGCC TTGGTAGGAT TGGGCCTGGG GATGTTTCAG CTCTTCCACC TACAGAAGGA    480
GCTGGCAGAA CTCGAGAGT CTACCAGCCA GATGCACACA GCATCATCTT TGGAGAAGCA    540
AATAGGCCAC CCCAGTCCAC CCCCTGAAAA AAAGGAGCTG AGGAAAGTGG CCCATTTAAC    600
AGGCAAGTCC AACGTCGAGG TTCTCCCTAT AGTGAGTCGT ATTAATTTCA GAGGAGTATT    660
TAGAAGAGAA GCTGAAGCTG TCGAGACA    688

```

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

```

GAATTCGGCC AAAGAGGCCT AATGATTTTG ATAGGAAGAA TGTCAGCCCA GGTTCCTCATG    60
AACATGACCA TCACAGGTTG TATGATGACG TTTTACAGGA CTACGCCGGC TGTGCTGTTT    120
TGGCAGTGGA TTAACCAATC CTTCAATGCC GTCGTCAATT ACACCAACAA AAGTGTGCGAG    180

```

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

```

GAATTCGGNC AAAGAGGCCT ACCACCTTCT CTGCCAGAAG ATACCATTTC AACTTTAACA      60
CAGCATGATC GAAACATACA ACCAACTTC TCCCCGATCT GCGGCCACTG GACTGCCCAT      120
CAGCATGAAA ATTTTATGT ATTTACTTAC TGTTTTCTT ATCACCAGA TGATTGGGTC      180
AGCACTTTT GGTGTGTATC TTCATAGAAG GTTGGNCAAG ATAGAAGATG AAAGGRAWYY      240
TYMATKRARR WTTTKKKWTY MWKRAACSR WWCARRRRW KSMAMMMRG RRRRRRWCC      300
YYWWCYTWC YTKRWSYTK KRRGRRRTW AAARCCMRKT TKGWRGGSYT TKKKRWGRW      360
TTWTWKKTW AAMMAMRRRG RRRMSRCGR RARRAAAMR CYTTTGNAAT NCNCCNAGGT      420
GATCAGAATC CTCACATTGC GGCACATGTC ATAAGTGAGG CCANCAGTAA AACAACATCT      480
GTGTTACAGT GGGCTGANAA AGGATACTAC ACCATGAGCA ACAACTTGGT AACCTGGAA      540
AATGGGAAAC AGCTGNCCGT TAAAAGACAA GGACTCTATT ATATCTATGC CCAAGTCGAG      600

```

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

```

NCCTGTTTCA TTAATTAAAT TTCCCGAAAG AACCTGAGTC ATTTTCCNAC ATGAGAATAC      60
TAGAAGAATG ACCAAGACTT GCGAGACGCG ATTTNCCGGG TGGTGCGAAC AATAGANCGA      120
CCATGACCTT GAAGGTGAGA CGCGCATAAC CGCTAGAGTA CTTTGAAGAG GAAACANCAA      180
TAGGTTGCTA CCAGTATAAA TAGACAGGTA CATACAACAC TGGAAATGGT TGTCTGTTG      240
AGTACGCTTT CAATTCATTT GGGTGTGCAC TTTATTATGT TACAATATGG AAGGGAACCT      300
TACACTTCTC CTATGCACAT ATATTAATTA AAGTCCAATG CTAGTAGAGA AG          352

```

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

```

GAATTCGGCC AAAGAGGCCT AAAGAAGACA AAGATGATAG GCGGCACAGA GATGACAAAA      60
GAGATTCCAA GAAAGAGAAA AAACACAGTA GAAGCAGAAG CAGAGAAAGG AAACACAGAA      120
GTAGGAGTCG AAGTAGAAAT GCAGGGAAAC GAAGTAGAAG TAGAAGCAAA GAGAAATCAA      180
GTAACATAA AAATGAAAGT AAAGAAAAAT CAAATAAACG AAGTCGAAGT GGCAGTCAAG      240
GAAGAACTGA CAGTGTGAA AAATCAAAAA AACGGGAACA TAGTCCCAGC AAAGAAAAAT      300
CTAGAAAGCG TAGTAGAAGC AAAGAACGTT CCCACAAACG AGATCACAGT GATAGTAAGG      360
ACCAGTCAGA CAAACATGAC CGTCGAG          387

```

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

GAATTCGGCC AAAGAGGCCT AAGGAAGTTG GATGTTTTGA TTTTACTGTT TATAGATGTT	60
AGATTGTACA GATTTGTCTG TATTTCTCAC CATATCTAAT GATACTTTTT TCATTAGATT	120
GGTCTTCAAG AACAGTATTA GTTATAATTA TTTTGTTTAT TCAGTATATA GTTAGCTCTT	180
ACAGTTTAGC TTTATTACCC ATATTTATAC TGTGGATTCA CAGCGAGAGG TAGAGGTTAT	240
TCCAGGAGAG TTGATGACCT TCATTTAAAG TCCAATAAAA ATCAGTAGTA GAAACATAAG	300
AAAACATCTT TGCAATATTT ACTTTTGTTT CTGTTTGCCG TAAATAGTAA CATTGTTTTT	360
TTTTATTTTG TGTTTGTAT AAAACAGTTG CATTACAAT ATTATTGGCC TGAGATATTG	420
ATGATATTGT GATGGTATGA AAATGTGTAC ATTCCCTGTG CAACATCAGA TTTGCAGGAA	480
AAATGAAGCA CTTACTGAAA TCGCTGGTAC TCGTCGAG	518

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 393 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

GAATTCGGCC AAAGAGGCCT AGGACAAAAC AAAACATTTT CCTTTGGGTT TTTTTTTTCT	60
TTCTTTTTTC TCCCCTTTAC TCTTTGGGTG GTGTTGCTTT TCCTTTCCTT TTCCCTTTGA	120
GATTTTTTTC TTGTTGTTTC CTTTTGTAT TTTACTGATA TCACCAGGAT AGTTTACTCT	180
CCTTCTAGCT TTCTGCTTAC CGCACACTGG ATAACACACA CATACACACC CACAAAATG	240
CTCATGAACC CAATCCGGAG AAGGTTCCAG CAGGTCCCCC ACCCTCCCCT CCTCCTCCTA	300
CTTCTCCTCT TGACAGCGAG GACAGGAGGG GGACAAGGGG ACACCTGGGC AGACCCGCCG	360
GCTCTCCCCC CACCCACCC CGGCACCTC GAG	393

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 421 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

GAATTCGGCC AAAGAGGCCT ACGAAGTTAC AGAACTGAGA TTCTCGGGTC CCAGACACGC	60
ACCTATGTAC CTCCCACTGG TGTCCCTGCA AAGCCTGGCG CTTTGTGACAT CAATAATAAA	120
AGTGGCAGGG CTGAGCAACA CCTCAGGAGT TACTCTGGAA GGATGGAGGA GTTATGTAAC	180
ACACGAGAGT CAGGAGCCCT GTGGAAGTGC TTTTATTAGC AGTAAGGCTG ATCGTACAAA	240
AAATCTCAG AGCTTCATAG GACAAGGTAG TACAAGTATG GATGATACAG GACTGAGGAA	300
CGGGGGACGG CTCAAAAGAA ATCAACATCG TCTGGGGCAT CCAGGTCCCG ATATTCCACA	360
ATGGCCCTTG GGTCTCCACG AACCATCCTG TGAGGTGAGA GGTACAGGAT CAGACCTCGA	420
G	421

(2) INFORMATION FOR SEQ ID NO:169:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 365 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

```

TAGGAGATCT GGATGGCATC TACTTCGTAT GACTATTGCA GAGTGCCCAT GGAAGACGGG      60
GATAAGCGCT GTAAGCTTCT GCTGGGGATA GGAATTCTGG TGCTCCTGAT CATCGTGATT      120
CTGGGGGTGC CCTTGATTAT CTTACCATC AAGGCCAACA GCGAGGCCTG CCGGGACGGC      180
CTTCGGGGAG TGATGGAGTG TCGCAATGTC ACCCATCTCC TGCAACAAGA GCTGACCGAG      240
GCCCAGAAGG GCTTTCAGGA TGTGGAGGCC CAGGCCGCCA CCTGCAACCA CACTGTGATG      300
GCCCTAATGG CTTCCTTGG ATGCAGAGAA GGCCCAAGGA CAAAAGAAAG TGAAGNATC      360
TCGAG

```

## (2) INFORMATION FOR SEQ ID NO:170:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

```

GAATTCGGCC AAAGAGGCCT AACACAGGAA ACATTACAAT TGAACAATGC CTCAGCTATA      60
CATTACATC AGATTATTGG GAGCCTATTT GTTCATCATT TCTCGTGTTC AAGGACAGAA      120
TCTGGATAGT ATGCTTCATG GCACTGGGAT GAAATCAGAC TCCGACCAGA AAAAGTCAGA      180
AAATGGAGTA ACCTTAGCAC CAGAGGATAC CTTGCCTTTT TTAAGTGCT ATTGCTCAGG      240
GCACTGTCCA GATGATGCTA TTAATAACAC ATGCATAACT AATGGACATT GCTTTGCCAT      300
CATAGAAGAA GATGACCAGG GAGAAACCAC ATTAGCTTCA GGGTGTATGA AATATGAAGG      360
ATCTGATTTT CAGTGCAAAG ATTCTCCAAA AGCCCAGCTA CGCCGGACAA TAGAATGTTG      420
TCGGACCAAT TTATGTAACC AGTATTGCA ACCCACGCTC GAG

```

## (2) INFORMATION FOR SEQ ID NO:171:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

```

GAATTCGGCC AAAGAGGCCT ACTTAGCTTC AAATCCCTAC TCCTTCACTT ACTAATTTTG      60
TGATTGGAA ATATCCGCGC AAGATGTGTA CGTTCAGAC TTGGCTAGTG CAAGCCTTGT      120
TTATTTTCTT CACCACTGAA TCTACAGGTG AACTTCTAGA TCCATGTGGT TATATCAGTC      180
CTGAATCTCC AGTTGTACAA CTTCACTTCTA ATTCACTGC AGTTTGTGTG CTAAAGGAAA      240
AATGTATGGA TTATTTTCAT GTAAATGCTA ATTACATTGT CTGGAAAACA AACCATTTTA      300
CTATTCCTAA GGAGCAATAT ACTATCATAA ACAGAACAGC ATCCACGCTC GAG

```

## (2) INFORMATION FOR SEQ ID NO:172:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

```

GAATTCGGCC AAAGAGGCCT ACACTCGTCT CTTTTTTTCC CCATCTCATT GCTCCAAGAA      60
TTTTTTTCTT CTTACTCGCC AAAGTCAGGG TTCCCTCTGC CCGTCCCGTA TTAATATTTT      120
CACTTTTGGG ACTACTGGCC TTTTCTTTT AAAGGAATTC AAGCAGGATA CGTTTTTCTG      180
TTGGGCATTG ACTAGATTGT TTGCAAAAGT TTCGCATCAA AAACAACAAC AACAAAAAAC      240
CAACAACCTC TCCTTGATCT ATACTTTGAG AATTGTTGAT TTCTTTTTTT TATTCTGACT      300
TTTAAAAACA ACTTTTTTTT CCACTTTTTT AAAAAATGCA CTACTGTGTG CTGAGCGCTT      360
TTCTGATCCT GCATCTGGTC ACGGTCGCGC TCAGCCTGTC TACCTGCAAC ACACTCGAG      419

```

## (2) INFORMATION FOR SEQ ID NO:173:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

```

GAATTCGGCC AAAGAGGCCT ACCCAGAAAC ATCCAATTCT CAAACTGAAG CTCGCACTCT      60
CGCCTCCAGC ATGAAAGTCT CTGCCGCCCT TCTGTGCCTG CTGCTCATAG CAGCCACCTT      120
CATTCCCCAA GGGCTCGCTC AGCCAGATGC AATCAATGCC CCAGTCACCT GCTGCTATAA      180
CTTCACCAAT AGGAAGATCT CAGTGCAGAG GTCGCGAGC TATAGAAGAA TCACCAGCAG      240
CAAGTGTCCT AAAGAAGCTG TGATCTTCAA GACCATGTGT GCCAAGGAGA TCTGTGCTGA      300
CCCCAAGCAG AAGTGGGTTC AGGATTCCAT GGACCACCTG GACAAGCAAC CCAAACCTCGA      360
G

```

## (2) INFORMATION FOR SEQ ID NO:174:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

```

TAGGACAAAA CAAACATTT TCCCTTGGGG TTTTTTTTTT CTTTCTTTT TCTCCCTTT      60
ACTCTTTTGG TGGTGTGCT TTTCCTTCC TTTCCTTTT GAGATTTTTT TGTTGTTGTT      120
TCTTTTTTGT ATTTTACTGA TATCACCAGG ATAGTTTACT CTCCTTCTAG CTTTCTGCTT      180
ACCGCACACT GGATAACACA CACATACACA CCCACAAAAA TGCTCATGAA CCAATCCGG      240
AGAAGGTTCC AGCAGGTCCC CCACCCTCCC CTCCTCCTCC TACTTCTCCT CTTGACAGCG      300
AGGACAGGAG GGGGACAAGG GGACACCTGG GCAGACCCGC CGGCTCTCCC CCCACCCAC      360
CCCGGCAC

```

## (2) INFORMATION FOR SEQ ID NO:175:



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

```

GAATTCGGCC AAAGAGGCCT AGACTAACCC AGAAACATCC AATTCTCAA CTGAAGCTCG      60
CACTCTCGCC TCCAGCATGA AAGTCTCTGC CGCCCTTCTG TGCCTGCTGC TCATAGCAGC      120
CACCTTCATT CCCCAAGGGC TCGCTCAGCC AGATGCAATC AATGCCCCAG TCACCTGCTG      180
CTATAACTTC ACCAATAGGA AGATCTCAGT GCAGAGGCTC GCGAGCTATA GAAGAATCAC      240
CAGCAGCAAG TGTCCCAAAG AAGCTGTGAT CTTCAAGACC ATTGTGGCCA AGGAGATCTG      300
TGCTGACCCC AAGCAGAAGT GGGTTCAGGA TTCCATGGAC CACCTGGACA AGCAAACCCA      360
AACTCCGAAG ACTTCACTCG AG

```

## (2) INFORMATION FOR SEQ ID NO:176:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

```

GAATTCGGCC AAAGAGGCCT AGTATAATAC TAAGTTGAGA TGATATCATT TACGGGGGAA      60
GGCGCTTTGT GAAGTAGGCC TTATTTCTCT TGTCCTTTCG TACAGGGAGG AATTGAAGT      120
AGATAGAAAC CGACCTGGAT TACTCCGGTC TGAAGTCAGA TCACGTAGGA CTTTAATCGT      180
TGAACAAACG AACCTTTAAT AGCGGCTGCA CCATCGGGAT GTCCTGATCC AACATCGAGG      240
TCGTAAACCC TATTGTTGAT ATGGACTCTA GAATAGGATT GCGCTGTTAT CCCTAGGGTA      300
ACTTGTCCG TTGGTCAAGT TATTGGATCA ATTGAGTATA GTAGTTCGCT TTGACTGGTG      360
AAGTCTTAGC ATGTACTGCT CGGAGGTTGG GTTCTGCTCC GAGGTCGCCC CAACCGAAAT      420
TTTTAATGCA GGTTCGGTAG TTTAGGACCT GTGGGTTTGT TAGGTACTGT TTGCATTAAT      480
AAATTAAAGC CTCGAG

```

## (2) INFORMATION FOR SEQ ID NO:177:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

```

TTNGGCCAAA GGGGCTTAGG ACAAACAAA ACATTTTCCT TTGGGTTTNA NTTTCTNTCT      60
TTNTTCTCCC ATTTANTNNT GGGGTGGTGT TGCTTTTCCT TTCCTTTTCC CTGGAGATT      120
TTNTNGTTGT NGTTTCCTTT TTGTATTNTA NTGATATCAC CAGGATAGTT TACTCTCNTT      180
NTAGCTNTGT GCTTACCGCA CANTGGATAA CACACACATA CACACCCACA AAAATGNTCA      240
TGAACCCAAT CCGGAGAAGG TTCCAGCAGG TCCCCCACC TCCCCTCCTC CTCNTACTTC      300
TCCTCTNGAC AGCGAGGACA GGAGGGGGAC AAGGGGACAC CTGGGCAGAC CCGCCGGCTN      360
TTCCCCCACC CCCACCCGG CACCCTCGAG

```

## (2) INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 356 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

```
GAATTCGGCC AAAGAGCAAT TCTCAAAC TG AAGCTCGCAC TCTCGCCTCC AGCATGAAAG      60
TCTCTGCCGC CCTTCTGTGC CTGCTGCTCA TAGCAGCCAC CTTCAATCCC CAAGGGCTCG      120
CTCAGCCAGA TGCAATCAAT GCCCCAGTCA CCTGCTGCTA TAACTTCACC AATAGGAAGA      180
TCTCAGTGCA GAGGCTCGCG AGCTATAGAA GAATCACCAG CAGCAAGTGT CCCAAAGAAG      240
CTGTGATCTT CAAGACCATT GTGGCCAAGG AGATCTGTGC TGACCCCAAG CAGAAAGTGGG      300
TTCAGGATTC CATGGACCAC CTGGACAAGC AAACCCAAAC TCCGAAGACT CTCGAG      356
```

## (2) INFORMATION FOR SEQ ID NO:179:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 480 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

```
GAATTCGGCC AAAGAGGCCT ACCGAGACTG ACACACTGAA CTCCACTTCC TCCTCTTAAA      60
TTTATTCTTA CTTAATAGCC ACTCGTCTCT TTTTTCCTCC ATCTCATTGC TCCAAGAATT      120
TTTTTCTTCT TACTCGCCAA AGTCAGGGTT CCCTCTGCCC GTCCCGTATT AATATTTCCA      180
TTTTTGGAAC TACTGGCCTT TTCTTTTAA AGGAATCAA GCAGGATACG TTTTCTGTGT      240
GGGCATTGAC TAGATTGTTT GCAAAAGTTT CGCATCAAAA ACAACAACAA CAAAAACCA      300
AACAACTCTC CTTGATCTAT ACTTTGAGAA TTGTTGATTT CTTTTTTTAA TTCTGACTTT      360
TAAAAACAAC TTTTTTTTCC ACTTTTTTAA AAAATGCACT ACTGTGTGCT GAGCGCTTTT      420
CTGATCCTGC ATCTGGTCAC GGTGCGCTC AGCCTGTCTA CCTGCAGCAC CACTCTCGAG      480
```

## (2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 462 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

```
GAATTCGGCC AAAGAGCCTA ACACAGGAAA CATTACAATT GAACAATGCC TCAGCTATAC      60
ATTTACATCA GATTATTGGG AGCCTATTTG TTCATCATTT CTCGTGTTCA AGGACAGAAT      120
CTGGATAGTA TGCTTCATGG CACTGGGATG AAATCAGACT CCGACCAGAA AAAGTCAGAA      180
AATGGAGTAA CCTTAGCACC AGAGGATACC TTGCCTTTT TAAAGTGCTA TTGCTCAGGG      240
CACTGTCCAG ATGATGCTAT TAATAACACA TGCATAACTA ATGGACATTG CTTTGCCATC      300
ATAGAAGAAG ATGACCAGGG AGAAACCACA TTAGCTTCAG GGTGTATGAA ATATGAAGGA      360
TCTGATTTTC AGTGCAAAGA TTCTCCAAAA GCCCAGCTAC GCCGACAAT AGAATGTTGT      420
```

CGGACCAATT TATGTAACCA GTATTGCAA CCCACGCTCG AG

462

## (2) INFORMATION FOR SEQ ID NO:181:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

GAATTCGGCC AAAGAGGCCT AACACAGGAA ACATTACAAT TGAACAATGC CTCAGCTATA	60
CATTACATC AGATTATTGG GAGCCTATTT GTTCATCATI TCTCGTGTTT AAGGACAGAA	120
TCTGGATAGT ATGCTTCATG GCACTGGGAT GAAATCAGAC TCCGACCAGA AAAAGTCAGA	180
AAATGGAGTA ACCTTAGCAC CAGAGGATAC CTTGCCTTTT TTAAAGTGCT ATTGCTCAGG	240
GCACTGTCCA GATGATGCTA TTAATAACAC ATGCATAACT AATGGACATT GCTTTGCCAT	300
CATAGAAGAA GATGACCAGG GAGAAACCAC ATTAGCTTCA GGGTGTATGA AATATGAAGG	360
ATCTGATTTT CAGTGCAAAG ATTCTCCAAA AGCCGAGCTA CGCCGGACAA TAGAATGTTG	420
TCGGACCAAT TTATGTAACC AGTATTGCA ACCCAGCTC GAG	463

## (2) INFORMATION FOR SEQ ID NO:182:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

TACGAGAAGT CCTGTAAGAC GTAAATATTT TTAAATTTCA CTGAATTTTT GTCTTTCTCG	60
GTACCATAGA ACACCACAGC CAAGAGATCT CGATCACTGC TTATGATCTT ACTGATGTAC	120
ACACTTTGGA TACACTGGAT GCTCATGTCA AAAGGTGTCA ACTCATCTTC ATCTCCATCC	180
TCTTCCTCAC CATCACCTTC TTCTTCTCCT TCCTCTTCCT CCCCACCTTC TTCCTCTTCT	240
TCGTCTACCT CATTGTGAGC CTCCTGCTCC CCATTTTCCT CATTAGCATT CCCGTTAGCA	300
GGGGCGTCTC TTCCATTTTC TGCCTCTTCC ACAACTTCCT TCTTCTCCTT TAAGTCCTTG	360
GTGGTGAGT	369

## (2) INFORMATION FOR SEQ ID NO:183:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

GAATTCGGCC NAAGANGCCT ATGATCNTCT TCTTTGAAGA AACATGAAGT TACACTATGT	60
TGCTGTGCTT ACTCTANCCA TCCTGATGTT CCTGACATGG CTTCCACAAT CACTGAGCTG	120
TNACAAAGCA CTCTGTGCTA NTGATGTGAG CAAATGCCTC ATTCAGGAGC TCTGCCNGTG	180
CCGGCCGGGA GAAGCAATTG CTCCTGCTGT NAGGAGTGCA TGCTGTGTCT TGGGGCCCTT	240

TGGGACGANT GCTGTGACTG TGTGGTATG TGTAATCCTC GAAATTATAG TGACACACCG 300  
CACCTCNAG 309

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

GAATTCGGCC AAAGAGGCCT AATTCTGGTT TAAGATTCTA TCCATTTCTC ACTCTCAGAT 60  
CTGTTTGTTT CACCCTCTCC CCCTAAATAT TTGGATTTTA TATAGACCAG TAGGCTAAGG 120  
TAGGGAAGAC CACTGACAAG TATAAATTTA AGAGTTTACA AAACCAAGGA GGCCATCCAG 180  
CCCCTAGTTC TAAGCCATGT TCAGCACAGT GCCAACTTTG CCTTCCCTGG CTGTCCTTGC 240  
TTGCTTTCTG GTTGCTGTAA TTCTGAGGGG CAACCAGGCT TGCTGTAGAG AGGAGAGCCA 300  
GATGATGTGG AAGCCTAAGG CCACACCCCT CGAG 334

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

TAACCAGCCT TGAAGAGCCC TTCCTCTGGC TTGCTAGGAA GCTCATTGGA GACCCTAACT 60  
TGGAATTTGT TGCCATGCCT GCTCTCGCCC CACCAGAAGT TGTCATGGAC CCAGCTTTGG 120  
CAGCACAGTA TGAGCACGAC TTAGAGGTTG CTCAGACAAC TGCTCTCCCG GATGAGGATG 180  
ATGACCTGTG AGAATGAAGC TGGAGCCCAG CGTCAGAAGT CTAGTTTAT AGGCAGCTGT 240  
CCTGTGATGT CAGCGGTGCA GCGTGTGTGC CACCTCATTA TTATCTAGCT AAGCGGAACA 300  
TGTGCTTCAT CTGTGGGATG CTGAAGGAGA TGAGTGGGCT TCGGAGTGAA TGTGGCAGTT 360  
TAAAAAATAA CTTTATTGTT TGGACCTGCA TATTTAGCTG TTTTGAACG CAGTTGATTC 420  
CTTGAGTTTC ATATATAAGA CTGCTGCAGT CACATCACAA TATTCAGTGG TGAATCTTGT 480  
TTGTTACTGT CATTCCCATT CCTTTTCGTT TAGAATCAGA AT 522

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

GAATTCGGCC AAAGAGGCCT AGGACAAAAC AAAACATTTT CCTTTGGGTT TTTTTTTTCT 60  
TTCTTTTTTC TCCCCTTTAC TCTTTGGGTG GTGTTGCTTT TCCTTTCCTT TTCCCTTTGA 120  
GATTTTTTTG TTGTTGTTTC CTTTTGTAT TTTACTGATA TCACCAGGAT AGTTTACTCT 180

CCTTCTAGCT TTCTGCTTAC CGCACACTGG ATAACACACA CATAACACACC CACAAAAATG	240
CTCATGAACC CAATCCGGAG AAGGTTCCAG CAGGTCCCCC ACCCTCCCCT CCTCCTCCTA	300
CTTCTCCTCT TGACAGCGAG GACAGGAGGG GGACAAGGGG ACACCTGGGC AGACCCGCCG	360
GCTCTCCCCC CACCCACCC CGGCACCCCTC GAG	393

## (2) INFORMATION FOR SEQ ID NO:187:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

GAATTCGGCC AAAGAGGCCT ATTCTAGGAC AAGAGCCAGG AAGAAACCAC CGGAAGGAAC	60
CATCTCACTG TGTGTAAACA TGACTTCCAA GCTGGCCGTG GCTCTCTTGG CAGCCTTCCT	120
GATTTCTGCA GCTCTGTGTG AAGGTGCACT TTTGCCAAGG AGTGCTAAAG AACTTAGATG	180
TCAGTGATA AAGACATACT CCAAACCTTT CCACCCCAA TTTATCAAAG AACTGAGAGT	240
GATTGAGAGT GGACCACACT GCGCCAACAC AGAAATTATT GTAAAGCTTT CTGATGGAAG	300
AGAGCTCTGT CTGGACCCCA AGGAAAATG GGTGCAGAGG GAGCTCGAG	349

## (2) INFORMATION FOR SEQ ID NO:188:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

GAATTCGGCC AAAGAGGCCT ACAAGAAAGC AAGCTCATCA TACTGGCTAG TGGTGACCC	60
CAAGCTTTAG TAAATATAAT GAGGACCTAT ACTTACGAAA AACTACTGTG GACCACAAGC	120
AGAGTGCTGA AGGTGCTATC TGTCTGCTCT AGTAATAAGC CGGCTATTGT AGAAGCTGGT	180
GGAATGCAAG CTTTAGGACT TCACCTGACA GATCCAAGTC AACGTCTTGT TCAGAACTGT	240
CTTTGGACTC TCAGGAATCT TTCAGATGCT GCAACTAAAC AGGAAGGGAT GGAAGGTCTC	300
CTTGGGACTC TTGTTGAGCT TCTGGGTTCA GATGATATAA ATGTGGTCAC CTGTGCAGAT	360
CTCGAG	366

## (2) INFORMATION FOR SEQ ID NO:189:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

TACAGCCACA TCTGGATACA CACACACACT CTTACATTCA TACCCAGAGA CTGGTGACACA	60
GACACACACA CATCCCCCGT CCTGCCAATC AGTCCCAGGA ACACACAGGT CTCTATCAAC	120
ACCCAGAAAT TCTGACACCA CAAGCACAGG CCAACCTACA GCTAGAGGAT TAATGTCCAG	180

ACCCACAGGC TGGTGTGCGC ATGTCCTTCC ACGTGAATGT CACATGGGAG GACAGACTGC	240
ATGGATTTT TTAATGACAC TATTTATTT ATTTTGTAG ACAGAGTCTC ACTCTGTCGC	300
CCAGGATGGA GTGCAGTGGC GTGATCTCGG CTCACTACAA CCTCCGCCTC CTGGGTTCAA	360
GCGATTCTCG TGCCTCAGCA TCCAAGTAC CTGGGATTAC AGGCGCATGC CACCACGTCC	420
A	421

## (2) INFORMATION FOR SEQ ID NO:190:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

GAATTCGGCC AAAGAGGCCT AGGGAGATCT GGATGGCATC TACTTCGTAT GACTATTGCA	60
GAGTGCCCAT GGAAGACGGG GATAAGCGCT GTAAGCTTCT GCTGGGGATA GGAATCTGG	120
TGCTCCTGAT CATCGTGATT CTGGGGGTGC CCTTGATTAT CTTCAACATC AAGGCCAACA	180
GCGAGGCCTG CCGGGACGGC CTTGGGCGAG TGATGGAGTG TCGCAATGTC ACCCATCTCC	240
TGCAACAAGA GCTGACCGAG GCCCAGAAGG GCTTTCAGGA TGTGGAGGCC CAGGCCGCCA	300
CCTGCAACCA CACTGTGATG GCCCTAATGG CTTCCCTGGA TGCAGAGAAG GCCCAAGGAC	360
AAAAGAAAAA GGAGGAGCTC GAG	383

## (2) INFORMATION FOR SEQ ID NO:191:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

GAATTCGGCC AAAGAGGCCT ACCCCAGTCC AGATCCAGGA CTGAGATCCC AGAACCATGA	60
ACCTGGCCAT CAGCATCGCT CTCCTGCTAA CAGTCTTGCA GGTCTCCCGA GGGCAGAAGG	120
TGACCAGCCT AACGGCCTGC CTAGTGGACC AGAGCCTTCG TCTGGACTGC CGCCATGAGA	180
ATACCAGCAG TTCACCCATC CAGTACGAGT TCAGCCTGAC CCGTGAGACA AAGAAGCACG	240
TGCTCTTTGG CACTGTGGGG GTGCCTGAGC ACACATACCG CTCCCGAACC AACTTCACCA	300
GCAAATACAA CATGAAGGTC CTCTACTTAT CCGCCTTCAC TAGCAAGGAC GAGGGCACCT	360
ACACGTGTGC ACTCCACCAC TCTGGCCATT CCCCACCAT CTCCTCCCAG AACGTCACCA	420
GTCTCGAG	428

## (2) INFORMATION FOR SEQ ID NO:192:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

GAATTCGGCC AAAGAGGCCT AAAGAGCTCT CACTTCAGTC TTACTTACCC CACTGCTATT	60
CCCTGTGGAG AAAGCCGGCT AATTGTTTGT ATAAGGCTAT CTGCCATTGT AGAATACCTT	120
TCTCTAGTAG CTGAATGACA ATCAACTATA CGTTCCATAC TAAACATGCC AGAGATAGGA	180
CTTTTAGGCC TTGCTTTACA AAAGTGGTTT TTAACAGCTG ACATGAATAT TTCCCGTTTC	240
TATTTCTTT TTTTTTTTTT TTTTTTTTTT TGAGACGGAG TCTCGCTCTA TCCCCACGC	300
TCGAG	305

## (2) INFORMATION FOR SEQ ID NO:193:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 0 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

## (2) INFORMATION FOR SEQ ID NO:194:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

GAATTCGGCC AAAGAGGCCT AANAGAAGAT GCCCCTGCTG ATCACTCTAA CCTGCTCCTC	60
TTCTGGCTCT CAGGCTACTC CATTGCCACT CAAATCACCG GTCCAACAAC AGTGAATGGC	120
TTGGAGCGGG GCTCCTTGAC CGTGCACTGT GTTACAGAT CAGGCTGGGA GACCTACTTG	180
AAGTGGTGGT GTCGAGGAGC TATTTGGCGT GACTGCAAGA TCCTTGTTAA AACCAGTGGG	240
TCAGAGCAGG AGGTGAAGAG GGACCGGGTG TCCATCAAGG ACAATCAGAA AAACCGCACG	300
TTCATGTGA CCATGGAGGA TCTCATGAAA ACTGATGCTG ACACTTACTG GTGTGGAATT	360
GAGAAAACCTG GAAATGACCT TGGGGTCACA GTTCAAGTGA CCATTGACCC AGCACCAGTC	420
ACCCAAGAAG AAACAGCAG CTCCCAACT CTGACCGGCC ACCACTTGGA CAACAGGCAC	480
AAGCTCCTGA AGCTCAGTGT CCTCCACCC CTCGAG	516

## (2) INFORMATION FOR SEQ ID NO:195:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

GAATTCGGCC AAAGAGGCCT AGCGCCCTGA AGACAGAATG TTCCATATCA GAGCTGTGAT	60
CTTGAGAGCC CTCTCCTTGG CTTTCCTGCT GAGTCTCCGA GGAGCTGGGG CCATCAAGGC	120
GGACCATGTG TCAACTTATG CCGCGTTTGT ACAGACGCAT AGACCAACAG GGGAGTTTAT	180
GTTTGAATTT GATGAAGATG AGATGTTCTA TGTGGATCTG GACAAGAAGG AGACCGTCTG	240
GCATCTGGAG GAGTTTGGCC AAGCCTTTTC CTTTGAGGCT CAGGGCGGGC TGGCTAACAT	300

TGCTATATTG AACAACTACT TGAATACCTT GATCCAGCGT TCCAACCACA CTCAGGCCAC	360
CAACGATCCC CCTGAGGTGA CCGTGTTC CAAGGAGCCT GTGGAGCTGG GCCAGCCCAA	420
CACCCTCATC TGCCACATTG ACAAGTTCTT CCTACCACTG CTCGAG	466

## (2) INFORMATION FOR SEQ ID NO:196:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 191 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

TAGGCAGAAT GGGACTCCAA GCCTGCCTCC TAGGGCTCTT TGCCCTCATC CTCTCTGGCA	60
AATGCAGTTA CAGCCCGGAG CCCGACCAGC GGAGGACGCT GCGCCAGGC TGGGTGTCCC	120
TGGGCCGTGC GGACCCTGAG GAAGAGCTGA GTCTCACCTT TGCCCTGAGA CAGCAGAATG	180
TGGATCGACG T	191

## (2) INFORMATION FOR SEQ ID NO:197:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 614 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

GAATTCGGCC AAAGAGGCCT AATGGATCTC ATGTGCAAGA AAATGAAGCA CTGTGGTTCT	60
TCCTCCTGCT GGTGGCGGCT CCCAGATGGG TCCTGTCCCA GCTGCAGCTG CAGGAGTCGG	120
GCCCAGGACT GGTGAAGCCT TCGGAGACCC TGTCCTCAC CTGCACTGTC TCTGGTGGCT	180
CCATCAGCAG TAGTAGTTAC TACTGGGGCT GGATCCGCCA GCGCCAGGG AAGGGGCTGG	240
AGTGGATTGG GAGTATCTAT TATAGTGGGA GCACCTACTA CAACCCGTCC CTAAGAGTC	300
GAGTCACCAT ATCCGTAGAC ACGTCCAAGA ACCAGTTCTC CCTGAAGCTG AGCTCTGTGA	360
CCGCCGCAGA CACGGCTGTG TATTACTGTG CGAGACATTC TGGGCGCAGC AGCTGGTTCA	420
CGTCCTACTG GGGCCAGGGA ACCCTGGTCA CCGTCTCCTC AGGGAGTGCA TCCGCCCAA	480
CCCTTTTCCC CCTCGTCTCN TGTGAGAATT CCCCGTCGGA TACGAGCAGC GTGGCCGTTG	540
GCTGCCTCGC ACAGGACTTC CTTCCCGACT CCATCACITTT CTCCTGGAAA TACAAGAACA	600
ACTCTGAACG CGAG	614

## (2) INFORMATION FOR SEQ ID NO:198:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 0 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

## (2) INFORMATION FOR SEQ ID NO:199:



- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 427 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

```
GAATTCGGCC AAAGAGGCCT ANACTGCAGC TCTTTTCATT TTGCCATCCT TTTCCAGCTC      60
CATGATGGTT CTGCAGGTTT CTGCGGCCCC CCGGACAGTG GCTCTGACGG CGTTACTGAT      120
GGTGCTGCTC ACATCTGTGG TCCAGGGCAG GGCCACTCCA GAGAATTACC TTTTCCAGGG      180
ACCGCAGGAA TGCTACGCGT TTAATGGGAC ACAGCGCTTC CTGGAGAGAT ACATCTACAA      240
CCGGGAGGAG TTCGCGCGCT TCGACAGCGA CGTGGGGGAG TTCCGGGCGG TGACGGAGCT      300
GGGGCGGCCT GCTGCGGAGT ACTGGAACAG CCAGAAGGAC ATCCTGGAGG AGAAGCGGGC      360
AGTGCCGGAC AGGATGAGCA GACACAATA CGAGCTGGGC GGGCCCATGA CCCTCACAGA      420
ACTCGAG                                         427
```

(2) INFORMATION FOR SEQ ID NO:200:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 322 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

```
TAGGGATGTC AACATGATCT TTTCATATAT GCTGGCTATA GAAATTGGTC TCGGTGAAGT      60
AATGGTCTGT CTGTCAAGCA TGACATCCTT GCCTGTGTTA AGTTTTGTGT GCTCTTCTGG      120
GATGTTGATC GTGACGTCTT TTCCGGGATT GAGAAGCTTC TGTTGCTCTT CTGGGATGTC      180
ATTCATGATC TCTTCATATA TGCTGGCTAT AGAAATTGGG CTCTGTGAAG AAATAGTGTG      240
TCCCAACCT TGGTACAGNC CCCCTGGGGA GGGTACCTTT GAAGAACCAG AAGTTAGANC      300
TTGTGAAGAA GAAGAAAGTA GG                                         322
```

(2) INFORMATION FOR SEQ ID NO:201:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 272 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

```
GAATTCGGCC AAAGAGGCCT ATGGAGTGTG AGAACAGCAA AAAATAATAA TTCAACCAGT      60
TGGTTATTAT GAACATCATT TTCTATTTTT TAAAAATATG CTATATCATG GAATTCAATG      120
TAAACCTCA AGAGATGCCA TCCTTGAGA GGGCTGCACC AGCCTGTGCC CCAAGTTACC      180
CAGGATCACC CCCTACTTCT CCTGACGGCC CCCCAGAGAA GGCCTGCATT CTGGGCGACG      240
TGGCCTTCAG GGGCTCAACC CTTGGCCTCG AG                                         272
```

(2) INFORMATION FOR SEQ ID NO:202:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

```
GAATTCGGCC AAAGAGGCCT AGCCAATTG GTTTTCTAAG TATTTTCACG CCTTCTCCTC      60
GTGTCCGCGT CACTGCTCTG ATTCAGGCCC TTGTCATTTT TCATCTTTGC CATTTTAGTA      120
GTTTTTGGAT TGGGCTCCCG GCTGCTAATT TTGTCCTTTC TTCCACTATC TTCCACATTG      180
TCACCGCAGT CATGTTTCTA AGGCAGAATC TCACTGTGCC CCACATCGTG TTGCTGGGCC      240
CTTGCAATGCC GTACCCCTGGC CTTTGTGAAA TGCCCTTCAT CTGTGCTCTT CCCTCCACCT      300
GGAATGTCCG TCTCTCTTTT TCTGCCAACC CACNCGACCC CTCCCTCCTN CAAGCCCGTG      360
AGTGTCCCN CCCTCCATGT CCTGTGGTGA CAGAGCTCGA G                               401
```

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

```
GAATTCGGCC AAAGAGGCCT ACGATATTTG CTGCGACCCG CAGGCGCTAT CCGCTGCCGG      60
GTTCTGGCGC GCCCTTTCAG TTCTGCTTGC TGTCGCACC GNTGCGTTAC CCGGAACCGC      120
CGGGCCGAAC AGCATGACGT CCGCTTTGGA GAACTACATC AACCGAACGT TTGCCGTTAT      180
TACATCAGAT GGGAGAATGA TTGTGGGAAC ACTGAAAGGT TTTGACCAGA CCATTAATTT      240
GATTTTGGAT GAAAGCCATG AACGAGTATT CAGCTCTTCA CAGGGGGTAG AACAAGTGGT      300
ACTAGGATTA TACATTGTAA GAGGTGACAA CGTTGCAGTC ATTGGAGAAA TCGATGAAGA      360
AACAGATTCT GCGCTTGATT AGGGGAACAC TCGAG                               395
```

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

```
GAATTCGGCC ANAGAGGCCT AAGAGCCAGT AAAAAAATTG TTAGAAAGCA GATACCATCA      60
AATTGGTTCT GGGAAAGTGT AAATCAAAGT TGCACAACCC AAAGAGGTAT ATAGGCAGCA      120
ACAGCAACAA CAAAAAGGTG GAAGAGGTGC TGCAGCTGGT GGACGAGGTG GTACGAGGGG      180
TCGTGGCCGA GGTCAAGGCC AAAACTGGAA CCAAGGATTT AATAACTATT ATGATCAAGG      240
ATATGGAAAT TACAATAGTG CCTATGGTGG TGATCAAAAC TATAGTGGCT ATGGCGGATA      300
TGATTATACT GGGTATAACT ATGGGAAC TAAGATATGGA CAGGGATATG CAGACTACAG      360
TGGCCAACAG AGCACTTATG GCAAGGCATC TCGAG                               395
```

(2) INFORMATION FOR SEQ ID NO:205:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 560 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

```
GAATTCGGCC AAAGAGGCCT AGTTTGGTCG TTCGTTGGGC GGTGCTGGTT TTTCGCTCGT      60
CGACTGCGGC TCTTCCTCGG GCAGCGGAAG CGGCGCGGCG GTCGGAGAAG TGGCCTAAAA      120
TTTCGGCGTT GGGTGAAAGA AAATGGCCCG AACCAAGCAG ACTGCTCGTA AGTCCACCGG      180
TGGGAAAGCC CCCC GCCAAA CAGTTGNCCA CGGAAANCCG CCAGGAAAAG CGCTCCNTCT      240
ACCGGCGGGG TGAAGAAGCC TCATCGCTAC AGGCCCGGGA CCGTGGCGCT TCGAGAGATT      300
CGTCGTTATC AGAAGTCGAC CGAGCTGCTC ATCCGGAAGC TGCCCTTCCA GAGGTTGGTG      360
AGGGAGATCC CGCAGGATT CAAAACCGAC CTGAGGTTTC AGAGCGCAGC CATCGGTGCG      420
CTGCAGGAGG CTAGCGAAGC GTACCTGGTG GGTCTGTTTC AAGATACCAA CCTGTGTGCC      480
ATCCACGCTA AGAGAGTCAC CATCATGCCC AAAGACATCC AGTTGGCTCG CCGGATACGG      540
GGAGAGAGAG CTTTCTCGAG
```

(2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 411 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

```
GAATTCGGCC AAAGAGGCCT ACTAGTTTAC TTTATCCCAT CCATTTATAT ATACATATAT      60
ATACACATAT ATGTGTGTTG TTTTGTGTTT GTTTGTTTTT GTTTTTTTGA GATGGAGTCT      120
CGCTCTGTCT CCCAGGCTGG AGTGCAGTGG TGTGATCTTG GCTCACTGCA ACCTCTGCCT      180
CCTGGGTTCA AGCAATTCTC CTGCCTCAGC TTCCCGAGT AGCTGGGACT ACAGGTGTGC      240
GCCACCACGC CCGGCAAATT TTTTTTTTTT TTTTTTTTTT TTGATATTTT TAGCAGAGAT      300
GAGGTTTCCC CACGTTGGCC AGGCTGGTCT CGAACTCTTG ACCTCAGGTT ATCTGCCTGC      360
CTTGGCCTCC CAAAGTGTG GATTACAGG CGTGAGCCAC CGAACCTCGA G      411
```

(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 0 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

(2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 411 base pairs  
 (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

GAATTCGGCC AAAGAGGCCT ACGTGGTGCG CGAGAGCGTA TCCCCAACTG GGACTTCCGA	60
GGCAACTTGA ACTCAGAACA CTACAGCGGA GACGCCACCC GGTGCTTGAG GCGGACCGA	120
GGCGCACAGA GACCGAGGCG CATAGAGACC GAGGCACAGC CCAGCTGGGG CTAGGCCCGG	180
TGGGAAAGGA GAGCGTCGTT AATTATTTC TTATTGCTCC TAATTAATAT TTATATGTAT	240
TTATGTACGT CCTCCTAGGT GATGGAGATG TGTACGTAAT ATTTATTTTA ACTTATGCAA	300
GGGTGTGAGA TGTCCCNCCT GCTGTAAATG CAGGTCTCTT GGTATTTAT GAGCTTTGTG	360
GGACTGGTGG AAGCAGGACA CCTGGAACCTG CGCCAAAGTA GGCGACTCGA G	411

(2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 152 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

GAATGCTGAT TGACCAGCTA AAAATCAAAT TACAAGATAG CCAAATAAC TTACAGATTA	60
ATGTATCTGA ACTTCAGACA TTGCAGTCTG AACATGNTAC ACTGCTAGAA AGGCACAACA	120
AGATGCTGCA GGAAACTGTG TCTCAGCTCG AG	152

(2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 355 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

GAATTCGGCC AAAGAGGCCT ACACNTCTGC ACCTCAACCA CAGACTACAC TTGCTGAACT	60
GGCTCCTGGG GCCATGAGGC TGTCACTGCC ACTGCTGCTG CTGCTGCTGG GAGCCTGGGC	120
CATCCAGGG GGCCTCGGG ACAGGGCGCC ACTCACAGCC ACAGCCCCAC AACTGGATGA	180
TGAGGAGATG TACTCAGCCC ACATGCCCGC TCACCTGCGC TGTGATGCCT GCAGAGCTGT	240
GGCTTACCAG GTGAGTCCTT CACCACTGTC ACCCTGCCCT GCTCACACCC CTTCTCAAGC	300
CAGACCCCTC CACCCACCTC ACATTCCACC ACCGGCCTTT GATCCCCGCC TCGAG	355

(2) INFORMATION FOR SEQ ID NO:211:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 403 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

GAATTCGGCC	AAAGAGGCCT	AATTATAAGC	ACTCAATAAT	ACATTATCAA	CTATTATTAC	60
TCAATTAAAA	CTGGTTAACT	TTAATTGAAT	TTGAACTGCC	ACCTAGAATA	GACAAGAAAA	120
TGAAACACAA	TTCTGTATGG	ATGTCAGAAA	CATGAAATAT	AAAATGTAAT	AAATAAAAAAT	180
ATTAAAAACC	CCTTAGCAAA	TGTTAAGGAG	CGTGTCAAAAT	GATTCCTGTG	TTGAACCTTA	240
AGCATTTAGG	TGGCTGGAGC	CTTGAAAGTT	ACCATCCCCC	AATTTTCTGC	TGTGCTACTA	300
GGTTTTTTTC	TATTGAGCAA	TTCTTTCAGG	TCGCCTCCAC	TCTGCTCTGC	CTAAAGGACA	360
ACTTCATATA	GTGCATTCTG	GTCTTAGACT	CCACGATCTC	GAG		403

## (2) INFORMATION FOR SEQ ID NO:212:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

GAATTCGGCC	AAAGAGGCCT	AAGCGCTAAG	CCTGGAGTGT	GGGCACTGCA	GTTTCAGAGG	60
CACCGATTAT	GAGAATGTGC	AGCTCCACAT	GGGCTCCATT	CATCCTGAGT	TCTGTGATGA	120
TATGGATGCC	GGGGGCCTGG	GCAAGCTCAT	CTTTTACCAG	AAGAGTGCAA	AGCTCTTCCA	180
TTGCCATAAG	TGCTTCTTCA	CCAGCAAGCT	GTACGCCAAT	GTGTACTATC	ACATCACGGC	240
CAGACACGCA	GCCTCGGACA	AGTGGAGTGA	GCAGCCGAAA	GAGCAGCCGA	GCAAAGACAC	300
CCGTCGAG						308

## (2) INFORMATION FOR SEQ ID NO:213:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

GAATTCGGCC	AAAGAGGCCT	ACTGTGGTAA	TTCTAGAGCT	AATACATGCC	GACGGGCGCT	60
GACCCCTTTC	GCGGGGGGGA	TGCGTGCAAT	TATCAGATCA	AAACCAACCC	GGTCAGCCCC	120
TCTCCGGCCC	CGGCCGGGGG	GCGGGCGCCG	GCGGCTTTGG	TGACTCTAGA	TAACCTCGGG	180
CCGATCGCAC	GCCCCCGGTG	GCGGCGACGA	CCCATTCGAA	CGTCTGCCCT	ATCAACTTTC	240
GATGGTAGTC	GCCGTGCCTA	CCATGGTGAC	CACGGGTGAC	GGGGAATCAG	GGTTCGATTC	300
CGGAGAGGGA	GCCTGAGAAA	CGTTACCAC	ATCCAAGGAA	GGCAGCAGGC	GCGCACCTCG	360
AG						362

## (2) INFORMATION FOR SEQ ID NO:214:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

GAATTCGGCC AAAGAGGCCT ATTCTTTTTT AAACAAATCA CCATATTGTA AATTCAGGG	60
TTTTTTTTTT GGTTTAAGCT GACTCTTNGC TCTAATTTTG GAAAAAAGA AATGTGAAGG	120
GTCAACTCCA ACGTATGTGG TTATCTGTGA AAGTTGCACA GCGTGGCTTT TCCTAAACTG	180
GTGTTTTTCC CCCGCATTG GTGGATTTT TATTATTATT CAAAAACATA ACTGAGTTTT	240
TTAAAGAGG AGAAAATTTA TATCTGGGTT AAGTGTATAT CATATATATG GGTACTTTGT	300
AATATCTAAA AACTTAGAAA CGGAAATGGA ATCTGCTCA CAAATCACT TTAAGATCTT	360
TTCGAAGCTG TTAATTTTTC CTAGTGTGTG GGACACTGCA GACTTGTCCA GTGCTCCAC	420
GGCCTGTACG GACACGACTC TCGAG	445

## (2) INFORMATION FOR SEQ ID NO:215:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

GAATTCGGCC AAAGAGGCCT ACTTCACTCT CTCATTCTTA GCTTGAATTT GGAAATGACT	60
TTTGATGACC TAAAGATCCA GACTGTGAAG GACCAGCCTG ATGAGAACTC AAATGGAAAA	120
AAAGCTAAAG GTCTTCAGTT TCTTTACTCT CCATGGTGGT GCCTGGCTGC TCGACTCTA	180
GGGGTCCTTT GCCTGGGATT AGTAGTGACC ATTATGGTGC TGGGCATGCA ATTATCCCAG	240
GTGTCTGACC TCCTAACACA AGAGCAAGCA AACCTAACTC ACCAGAAAAA GAACTGGAG	300
GGACAGATCT CAGCCCGCA ACAAGCAGNA GAAGCTGTTT TCGAG	345

## (2) INFORMATION FOR SEQ ID NO:216:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

GAATTCGGCC AAAGAGGCCT ACTGGGGAGT CTGCTATATT GTTGTTAAGG TCTCTTTGTT	60
AGTGGTGGTA GAAATTGGAG TATCCCTCTC CATTGTGGT TGGTGGCTGG ATATCTGTTT	120
CTTGAAATG TTTGATGCTA CTCTGAAAGA TCGAGAACTG AGCTTTCAGT CGGCTCCAGG	180
TACTACCATG TTTCTGCATT GGCTAGTGGG AATGGTATAT GTCTTCTACT TTGCCTCCTT	240
CATTCTATTA CTGAGAGAGG TACTTCGACC TGGTGTCTTG TGGTTTCTAA GGAATTTGAA	300
TGATCCAGAT TTCAATCCAG TACAGGAAAT GATCCATTTG CCAATATATA GGATCTCCG	360
AAGATTTATT TTGTCACTGA TTGTCTTTGG CTCCATTGTC CTCCTGATGC TTTGGCTTCC	420
TATACGTATA ATTAAGAGTG TGCTGCCTAA TTTTCTTCCA TACAATGTCA TGCTCTACAG	480
TGATGCTCCA GTGAGTGAAC TGTCCCTCGA G	511

## (2) INFORMATION FOR SEQ ID NO:217:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

```
GAATTCGGCC AAAGAGGCCT AGTTTATACC CACAGAATTT TTTCATAAAA TTAACCAAAC    60
CCTTTTCACT TTGCTTAAGA CTTCACTTTT GTCCCATTAC TCTTTAAGGT TAAGACCATC    120
TATAAAATCC TCTGAAGTGG ACAAATTTAC ATTCTCTTTA NCAAAATCCA TATTCCTATG    180
CCTTCTTATA ATCTTTTACC AAAAACACCT TCCCTATACA CCTTGTACGT AAAACTGTTT    240
CTCCAGTGGT CTCAACTACA TATTATACTG TTAACCTCTA CTCCTTTTAG CATAGCTAGT    300
AGGCATGGCT CTCCATATGT TCCCAGGCAT CTCGAG                                336
```

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

```
GAATTCGGCC AAAGAGGCCT AGTGGGTAGA TACAGACCCT AACTTTGAGC TCTAAGATGA    60
AATTTGTTTA TAAATCCCTA GTTCCATTG AGTTTTCATCA ATATTATCA AACACCTACT    120
GTGCCAGGCA TTGTTTAGGC ACAGGGGATA CAGCAGAAAA ACTCGAG                                167
```

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

```
GAATTCGGCC AAAGAGGCCT ACACACGCCT TTGGCACAAT GAAGTGGGTA ACCTTTATTT    60
CCCTTCTTTT TCCTTTTAGC TCGGCTTATT CCAGGGGTGT GTTTCGTGCA GATGCACACA    120
AGAGTGAGGT TGCTCATCGG TTTAAAGATT TGGGAGAAGA AAATTTCAAA GCCTTGGTGT    180
TGATTGCCTT TGCTCAGTAT CTTCAGCAGT GTCCATTGTA AGATCATGTA AAATTAGTGA    240
ATGAAGTAAC TGAATTTGCA AAAACATGTG TTGCTGATGA GTCAGCTGAA AATTGTGACA    300
AATCACTTCA TACCCTTTT GGAGACAAAT TATGCACAGT TGCAACTCTT CGTGAAACCT    360
ATGGTGAAAC CCTCGAG                                377
```

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

CTTGGGGGTG	GGTTCNNNT	ANNAAAAATT	ANAGNCGTTG	GGGGTTGGGG	GGCNGAGAAG	60
GAANANAGAA	CCCCNGGNAA	AATTTGAAAA	CNGGGTNATT	TATCCNGTNT	TTTNAANGAG	120
AATCCCANNC	CCGGAAAAAA	AAAAAAAANG	AGGAANANAN	AGATTGTAAG	TTAAAACAAA	180
AATCTATCTG	TATAAGTCTT	TACTTGTACA	AGTCTGTACA	AGTCAGTNAG	GTTTGGTCTC	240
TGCAGAGCCA	GAAGGTCAGA	GAAGGTGATT	TAATTGTAGG	CNTCTTTGGT	AGGCCTCTTT	300
GGCCGAATTC						310

## (2) INFORMATION FOR SEQ ID NO:221:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

GAATTCGCCC	AAGAGGCCTA	AAGAGGCCTA	GAAGCCAAAA	AACTTTCCCT	GAAAGGAGTC	60
TTCACCAAAG	AGCTCCCATC	TGGCAAGAAA	TACCTCCGCT	ACACACCCCA	GCCTTAAGTC	120
TCTTGAGAA	GCTGGTGCTG	TGAGCCAGAG	GATGTCAGCT	GCCAATTGTG	TTTTCCTGCA	180
GCAATTCCAT	AAACACATCC	TGGTGTATC	ACAGCCAAGG	TTTTTAGGTT	GCTATACCAA	240
TGGCTTATTA	AATGAAAATG	GCACTAAAAG	TTCTTGAGA	TTCTTTATAC	TCTCTGCCTT	300
CAGCAATCTC	GAG					313

## (2) INFORMATION FOR SEQ ID NO:222:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

GAATTCGGCC	AAAGAGGCCT	AGGAACCACT	GGCTGGTG	ATTTTGCTAG	ATTTTCTGA	60
TTTTTAAACT	CCTGAAAAAT	ATCCAGATA	ACTGTCATGG	AGCTGGTAAC	TATCTTCCTG	120
CTGGTGACCA	TCAGCCTTTG	TAGTTACTCT	GCTACTGCCT	TCCTCATCAA	CAAAGTGCCC	180
CTTCCTGTTG	ACAAGTTGGC	ACCTTTACCT	CTGGACAACA	TTCTTCCCTT	TATGGATCCA	240
TTAAAGCTTC	TTCTGAAAC	TCTGGGCATT	TNTGTTGGGC	ACCTTGTTGA	GGGGCTAAGG	300
AAGTGTTAA	ATGAGCTGGG	ACCAGAGGCT	TCTGAAGCTG	TGGAGCAACC	GCTCGAG	357

## (2) INFORMATION FOR SEQ ID NO:223:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

GAATTCGGCC	AAAGAGGCCT	ATTAAATGTG	TCATTGGAAG	CCATCCCTTT	TTTACATT	60
CATACAACAG	AAACCAGAAA	AGCAATACTG	TTCCATTTT	AAGGATATGA	TTAATATTAT	120



TAATATAATA ATGATGATGA TGATGATGAA AACTAAGGAT TTTTCAAGAG ATCTTTCTTT	180
CCAAAACATT TCTGGACAGT ACCTCGAG	208

## (2) INFORMATION FOR SEQ ID NO:224:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

TNAAACCAAT AGTTTTTTAA AAGACAAGCT TGGGTGGGTG CANGNTGGGG ACAGTGCTGG	60
TCTTTCACNG CAGCCCAGGC ACCNNTTGAG AGTCCCAGNG NGNGTNATGC CCGAGCCAG	120
TNAAGATGAA GGGAGAGCGG GTGCGGGGGC CATCNTCGGN GTCCCAGCCC GGCCCATGGG	180
ANTGAGTNGC GGCCTCTGCT TGTCGACNTG GGNGCTGGCT GTCCNATTTT ACTACTATTG	240
ACCCCTGAAGG CCATCGAGGA GGGCAGCATG GAGGAGATCG AAGAGGAGGT CCGGCAGAAG	300
AAATCATCAC GGAAGCGCAA GCGAGACTAG GCNTCTNTGG CCGAATTC	348

## (2) INFORMATION FOR SEQ ID NO:225:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

GAATTCGGCC AAAGAGGCCT ACTTCTCTG CAGATCATGG GGGCCTTGAT TGTGCTGTG	60
GGATTGTGTT TCTTCGTGGT TGCCCATGTT AAGAAGAGAA ACACGCTGAA TGCTGGCCAG	120
GATGCCTCTG AGAGAGAAGA GGGACAGATC CAGATTATGG AGCCTGTCCA GGTCACTGTA	180
GGTGACTCGG TAATAATATT TCCACCCCTT CCACCACCTT ACTTTCCTGA ATCTTCAGCT	240
TCTGCGGTCG CTGAGAGTCC TGGAACTAAC AGTCTGCTTC CGAATGAAAA CCCCCCTTCA	300
TATTACAGTA TTTTCAACTA TGGCAGGACC CCAACTTCAG AGGGTGACGC CTCTGAAAGA	360
GATTGTGAAT CTATATATAC CATTCTGGG ACGAATTCAT CTTCTGAGGC CTCACACACT	420
CCACATCTTC CATCTGAATT GCCTCCTAGA TATGAAGAAA AAGAAAATGC TGCAGCACTC	480
GAG	483

## (2) INFORMATION FOR SEQ ID NO:226:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

GAATTCGGCC AAAGAGGCCT ACGATTACAA TCATGATTTC CAGAATGGAG AAGATGACGA	60
TGATGATGAA GATATTGATT ATGTTTGCTC TTGGAATGAA CTACTGGTCT TGCTCAGGTT	120
TCCCAGTGTA CGACTACGAT CCATCCTCCT TAAGGGATGC CCTCAGTGCC TCTGTGGTAA	180

AAGTGAATTC CCACTCACTG AGTCCGTATC TGTTCGGGC ATTCAGAAGC TCATTAAAAA	240
GAGTTGAGGT CCTAGATGAG AACAACTTGG TCATGAATTT AGAGTTCAGC ATCCGGGAGA	300
CAACATGCAG GAAGGATTCT GGAGAAGATC CCGCTACATG TGCCTTCCAG AGGGACTACT	360
ATGTGTCCAC AGCTGTTTGC AGAAGCACCG TGAAGGTATC TGCCCAGCAG GTGCAGGGCG	420
TGCATGCTCG CTGCAGCTGG TCCTCCTCCA CGTCTGAGTC TTACAGCAGC GAAGAGATGA	480
TTTTTGGGGA CACTCTCGAG	500

## (2) INFORMATION FOR SEQ ID NO:227:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

GAATTCGGCC AAAGAGGCCT AGGAGAAAGA AGATATTGAC ACCATCTACG GGCACCATGG	60
AACTGCTTCA AGTGACCATT CTTTTCTTC TGCCAGTAT TTGCAGCATT AACAGCACAG	120
GTGTTTTAGA GGCAGCTAAT AATTCATTG TTGTTACTAC AACAAAACCA TCTATAACAA	180
CACCAAACAC AGAATCATT CAGAAAAATG TTGTCACACC AACAACTGGA ACAACTCCTA	240
AAGGAACAAT CACCAATGAA TTACTIONAAA TGCTCTGAT GTCAACAGCT ACTTTTTTAA	300
CAAGTAAAGA TGAAGGATTG AAAGCCACAA CCACTGATGT CAGGAAGAAT GACTCCATCA	360
TTTCAAACGT AACAGTAACA AGTGTTACAC TTCCAAATGC TGTTCACAA TTACAAAGTT	420
CCAAACCCAA GACTGAAACT CAGAGTTCAA TTAACAAC AGAAATACCA GGTAGTGTTT	480
TACAACCAGA NCTCGAG	497

## (2) INFORMATION FOR SEQ ID NO:228:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

GAATTCGGCC AAAGAGGCCT ACTTTTTTAA TATAAATTTT GTTGATATGG AATTAGGTAA	60
GTTTAAAGTGT CTATGTGCAT ATGTTTTTTA TATAAGTTT TTCTATTCA TTTACNGAT	120
CCAACTGGCA GTGGTAAAT ATGGCGAGCT CGAG	154

## (2) INFORMATION FOR SEQ ID NO:229:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

GAATTCGGCC AAAGAGGCCT AGGAATGGTT TTNATTGGT CCTTATTTT AACCTGCCCC	60
TGAGACTTAT ATGCTTGTTT ATACCATGTA CGTAGTGTGT GATTGTATGT GTTTGTATTT	120

GTCCACATGT CCCAAAACAT GGGCTGTTAC TCCCTTTTCT ATCTTGTTTT CCTTATTCCC	180
ACCCCTTCTCT TTCCACCCAG GTATCTGGAC AGGAAGACTT CTACCATCAG CTTTACCAGA	240
GGAAGCTGCA GGCCCCACTG TGGCCCAGCT CCTGGGCAT CACTGATTGC TATCAGTATG	300
TCACCTCCTG TCACCCCAAG AGATCAGAGA GACGCAAGTA TGGCCGAGAC TTCCTGCTAC	360
GTTTCCGCTT CTGCAGCATC GCTCGAG	387

## (2) INFORMATION FOR SEQ ID NO:230:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

GAATTCGGCC AAAGAGGCCT ACCTTCATTT GTTAGATTAT ATCAGTACCC CAACTTTGCT	60
GGACCTCATG CAGCTTTAGC TAATAAAAGT TTCTTTAAGG CAGATAAAGT TACAATGCTG	120
TGGAATAAAA AAGGTATGTT AAGTATATTT TATCCCTCCC TTTGTTTATC AGTTGTAAAT	180
TTAGGCTATA TTCCTATGTG TATAACAGAA GAATCAATGC CCATTGTGT TTTAAATCTA	240
ATTAAAGTTT TTAGTGTAT AGCTACTGCT GTGTTGGTAA TAGCTAGCAC AGATGTTGAC	300
AAGACAGGAG CTTCTACTA TGGAGAACGA CTCGAG	336

## (2) INFORMATION FOR SEQ ID NO:231:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

GAATTCGGCC AAAGAGGCCT AGGGACATTG GTTGAATTGG CATGACTAGA ATAGTTGGGA	60
ATGTTTGGGA ATGGGAGAG ATTGCTAATG GGATGTCTGC CAGGGGCAAT ACTGAAATCT	120
GCTGGTTGGT AAAGGTAGTG CCTGAGCCCA GTGCTAACCA TAGTAGTTGG AAAATTGTGT	180
ACGTTGGCTG TGGAAATCCTT ATGCGAATAT TTGTCCAATC CATCTAAATT TCTCTCTGCA	240
GCATTTTAA AAAGACATAT AGCTGAAAT TGTGAGTCC TAAAAATATT TTGTATTCT	300
CTGCCAGAT TTGCATTGG GTAGATCGTG CTGTAGAAGA TATATCTGC TTTAAGATAG	360
CTGCCACTGA TTAGTTTATT TTAGTCTATT TTAATCAACT TATTGCCTTG TAATCTTTCC	420
TTTTTCATT TCTAAATTC TGAAATTCTA TCTTCATGT TCCCCAGGAA AACTCGAG	479

## (2) INFORMATION FOR SEQ ID NO:232:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

GAATTCGGCC TTCATGGCCT ACATGATGTC AACACCGTG GCTCACAAGA TGAAAGAGCA	60
--	----

CATTCCTTTT TTTGAAGATA TGTGTAAAGG CATTAAAGCT GGTGACACCT GTGAGAAGCT	120
GGTGGGATAT TCTNCCGTGT ATAGAGTCTG TTTTGGAATG GCTTGTTTCT TCTTTATCTT	180
CTGTCTACTG ACCTTGAAAA TCAACAACAG CAAAAGTTGT AGAGCTCATA TTCACAATGG	240
CTTTTGTTT CTTTAACTT CTGCTGTTGG GGGCCATGTG CTCAGGAGCT TTCTTCATTC	300
CAGATCAGGA CACCTTTCTG AACGCCGGGC AGCTCGAG	338

## (2) INFORMATION FOR SEQ ID NO:233:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

GAATTCGGCT TCATGGCCTA CCCCGAACCA CTCAGGGTCC TGTGGACAGC TCACCTAGTG	60
GCAATGGCTC CAGGCTCCCG GACGTCCCTG CTCCTGGCTT TTGCCCTGCT CTGCCTGCCC	120
TGGCTTCAAG AGGCTGGTGC CGTCCAAACC GTTCCGTAT CCAGGCTTTT TGACCACGCT	180
ATGCTCCAAG CCCATCGCGC GCACCAGCTG GCCATTGACA CCTACCAGGA GTTTGAAGAA	240
ACCTATATCC CAAAGGACCA GAAGTATTCA TTCCTGCATG ACTCCAGAC CTCCTTCTGC	300
TTCTCAGACT CTATTCCGAC ACCCTCCAAC ATGGAGGAAA CGCAACAGAA ATCCAATCTC	360
GAG	363

## (2) INFORMATION FOR SEQ ID NO:234:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

GAATTCGACC TTCATGACCT AGCGTAAGAG GAGAGAGACA CATTGAGCAG CCAAAGGACT	60
CGGTGGAAAG AGCAGAACAC CATAGACAAT ATGTCGCTCT TGGGACCCAA GGTGCTGCTG	120
TTTCTTGCTG AATTCATCAT CACCTCTGAC TGGATACCCC TGGGGGTCAA TAGTCAATCG	180
AGGAGACGAT GTGACTCAAG CGACTCCAGA AACATTGACA GAAGATCCTA ATCTGGTGAA	240
TGATCCCGCT ACAGATGAAA CAGTTTGGC TGTTTTGGCT GATATTGCAC CTTCCACAGA	300
TGACTTGGAG TGCTGGGATG AGAAATTAC CTGCAGCAAG GCTCTACTCT GTGCATCGGC	360
CGGTAAACT CGAG	374

## (2) INFORMATION FOR SEQ ID NO:235:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

GAATTCGGCC TTCTGGCCTA GGGTGGGATA AGTGATTNGT ATTTGTTNG GTTTAAAAAC	60
--	----

ATACTTTGAT AGAAATTAGT CCCTTCTTT TCCTTCTCTT CTACAATGTC AATTGCCCAT	120
TTCATTTGTG TGTTCTAAC ATTTTCTTTT GTTAAGAAAT GTTGGGGCTA TAATTTT	180
GAAATCACTG AAGGAGGGG AAAAATAATT TTAACAACCT GTGTTGAAAC CTTCCATAGC	240
TTAATTGACT GGAATAATCC TGCCATCATT AATAAGATGT ACAAGGTGTA CCTTGAGAT	300
ATACCACTGA AGACANAGA GGAGCTCGAG	330

## (2) INFORMATION FOR SEQ ID NO:236:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 107 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

TTACACCCTG GAAACCAAGC ATAAGCACAC TTTAGCAGA TGACTTAGAA ATTAAGTTGT	60
TTGAATCNAG TGAACACACT GAAGACTCCA ACAACCCACA ACTCGAG	107

## (2) INFORMATION FOR SEQ ID NO:237:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 338 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

GAATTCGGCC TTCATGGCCT ACCCGTCGTT AGTGAAGGGG AAATGGGTTG TATCCTAAGG	60
GATTGGGAAA TGGGAAGTGA ATTTGAGGAG ATTGTGGAGT ACAAGGTATG TGTTTACGTT	120
AGGTGATGAG CAGTGTGAGG ATAGTGAAGT GTGGACAGTG TCAAATGCTT TTCTGTAGGG	180
AAGATGAAGT TAGCATCATC TTATCACTTT TGACATGCTT TTGTGGTTTA TTTTGTGTTG	240
TATTTGTTTT TTAGTAGAAA TGAAAGGCTT TGCCAAAGCC TCTGTACTAT GCTTCAGAGT	300
AGGACACACA ATTCTGAGAT TGCTGTAGAG GGCTCGAG	338

## (2) INFORMATION FOR SEQ ID NO:238:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 455 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

GAATTCGGCC TTCATGGCCT AGTCAGAGCC AAAGGAAAGC TTGAAAAATG AAGACATTAG	60
CAGGACTTGT TCTGGGACTT GTCATCTTTG ATGCTGCTGT GACTNCCCCA ACTCTAGAGT	120
CCATCAACTA TGACTCAGAA ACCTATGATG CCACCTTAGA AGACCTGGAT AATTTGTACA	180
ACTATGAAAA CATACCTGTT GATAAAGTTG AGATTGAAAT AGCCACAGTG ATGCCTTCAG	240
GGAACAGAGA GCTCCTCACT CCACCCCCAC AGCCTGAGAA GGCCCAGGAA GAGGAAGAGG	300
AGGAGGAATC TACTCCCAGG CTGATTGATG GCTCTTCTCC CCAGGAGCCT GAATTCACAG	360
GGGTTCTGGG GCCACACACA AATGAAGACT TTCCAACCTG TCTTTTGTGT ACTTGATAA	420

GTACCACCGT GTACTGTGAT GCCCATGAAC TCGAG

455

## (2) INFORMATION FOR SEQ ID NO:239:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

```

GAATTCGGCC AAAGAGGCCT AGGGGGGTGA TGGTGTGTGC TTTGGACTGT GTGCCTACAG      60
GGTTTTTTTG TTTTGTTTTG TTTTACTGTA ATGGAAATGG GTTTAGGATA AGCATACTCA      120
AAGCTCCACA GTGTATCCTT GAGCTTTCCA TGACTGCCAG TTACACACTG GAGAGGGTTA      180
AATGAATCTT AAAGTGTTCA TGATTACTAT TAAATATCAT TATAAAACAA ATTCTTTCGG      240
GGGGGCACAA ATGCTAATAT GTACAAGAAA ATCTTAGACT TGAAAATATC TTAAAAATGA      300
AAATAACTTT TTTTTCAGC TGACTGTATT CACAACCTTG ATGGATGTTA CCAAAGGTCA      360
ATTTGAAAGT CACCTTCGAG ATTGCCCGA CCCTGTGATA GGCTGGTGAG CACACGTTGG      420
CCAGCCTCGA G                                     431

```

## (2) INFORMATION FOR SEQ ID NO:240:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

```

GAATTCGGCC TTCATGGCCT ACTACAATCC GTGGGTGCTC NTTCTTGCCT ACTTTACTCT      60
CCCACTGAAG CAGGTTANCG TTGAAGGTGG TATGGAAAAG CCTGCATGCC TGTTCATTC      120
TTTTGTTTCT TCTCCTTCCC CCTCCCCCTA CCTCCTTCCC CTACCTCCTT CGCTCGAG      178

```

## (2) INFORMATION FOR SEQ ID NO:241:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

```

GAATTCGGCC TTCATGGCCT ACATCAACAG CATCAAGTCC AGACTAAGCA AAAGTGGGCA      60
CATACAACT CTGCTTAGAG CATTGGAAGC TCGTGATCGA AACATACAAG AAAGCAACTT      120
TGATAGAGTC AATTCTGGT CTATGGTTAA TTAGTGGTC ATGGTGGTGG TGTGAGCCAT      180
TCAAGTTTAT ATGCTGAAGA GTCTGTTTGA AGATAAGAGG AAAAGTCTCG AG          232

```

## (2) INFORMATION FOR SEQ ID NO:242:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

```
GAATTCGGCC TTCATGGCCT ACAAACCTA ACTTCGCGAG AAAACAAGAT GAGATTGGCA    60
TGGCTTTATT TGTTTTTTT GTTTGTTTT GGTTTTTTTT TTTTTTTTGG CTTGACTCAG    120
GATTTAAAAA CTGGAACGGT GAAGGTGACA GCAGTCGGTT GGAGCGAGCA TCCCCCAAAG    180
TTCAGTGGGC TCGAG                                                    195
```

(2) INFORMATION FOR SEQ ID NO:243:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 325 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

```
GAATTCGGCC TTCATGGCCT ACATATCCTC AAATGGTAGT CATCTGGGGA CTAAGCAACA    60
GGTGTTCCTAA GGAAGTAATT CTCTGGGTTT GAAAAGTTCA CAGTCTGTGC AGTCTATTCTG    120
TCCTCCATAT AACCGAGCAG TGTCTCTGGA TAGCCCTGTT TCTGTTGGCT CAAGTCCTCC    180
AGTAAAAAAT ATCAGTGTCT TCCCCATGTT ACCAAAGCAA CCCATGTTGG GTGGGAATCC    240
AAGAATGATG GATAGTCAGG AAAATTATGG CTCAAGTATG GGAGACTGGG GCTTACCAAA    300
CTCAAAGGCC GGCAGCGGAC TCGAG                                                    325
```

(2) INFORMATION FOR SEQ ID NO:244:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 342 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

```
GAATTCGGCC TTCATGGCCT AGGAGGCTAT TTAGGATTT CAATGAGAAG CAAAATCATA    60
TCCAAATCAA AGTAAAGGTC ATCGGTGGCC AATGAAGAGC GGAGAAAACG GAGGCGGGAG    120
AACAGACGCG ACCTCAAGAC AGAAGAATGG AAGACGCAAC TTTCAAGAAA AGAGGAACTG    180
AAACGAAAAG AGAGGCACAG TCCAAATGAG GAAGAGAACA AGGAGCCTTC AGTCTCCTGG    240
GGGCCAGGGA GCCTCGCCAC GCGGTCACAG GTACACGGGG ACATTAGAG GCCATCTCCT    300
TTAAAGCCAG ACATTCTTCT TACTGGAATC TAGGCCATGA AG                                                    342
```

(2) INFORMATION FOR SEQ ID NO:245:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 373 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

GAATTCGGCC TTCATGGCCT AGGCGGGTGA CATTCAGCCG GCGGTTGGG GGGACGGANT	60
CTCCATTCCA GAACCATGGC CCAATTTGTC CGTAACCTTG TGGAGAAGAC CCCGGCGCTG	120
GTGAACGCTG CTGTGACTTA CTCGAAGCCT CGATTGGCCA CATTTTGGTA CTACGCCAAG	180
GTTGAGCTGG TTCCTCCAC CCCTGCTGAG ATCCCTAGAG CTATTAGAG CCTGAAAAAA	240
ATAGTCAATA GTGCTCAGAC TGGTAGCTTC AACAGCTCA CAGTTAAGGA AGCTGTGCTG	300
AATGTTTGG TGGCCACTGA GGTGTTGATG TGGTTTATG TCGGAGAGAT TATAGGCAGG	360
CGGGTCACTC GAG	373

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

GAATTCGGCC TTCATGGCCT AAACAGGACC TGCTTCACAC CACCAAGCAT CAGGATGTGT	60
TGCTCAGTGA GCAGACCCGA CTCCAGAAGG ACATCAGTGA ATGGGCAAAT AGGTTTGAAG	120
ACTGTCAGAA AGNAGAGGAG ACAAACAAC AACAATTCA AGTGCTTCAG AATGAGATTG	180
AAGAAAACAA GCTCAAATA GTCCAACAAG GAAATGATGT TTCAGAGACT CCAGAAAGAG	240
AGAGAAAGTG AAGAAAGCAA ATTAGAAACC AGTAAAGTGA CACTGAAGGA GCAACAGCAC	300
CAGCTGGAAA AGGAATTAAC AGACCAGAAA AGCAAAGTGG ACCAAGTGCT CTNCAAAGGT	360
GCTGGCAGCT GAAGAGCGTG TTAGGACTCT GCAGGAAGAG GAGAGGTGGT GTGAGAGCCT	420
GGAGAAGACA CTCTCCCAA CTAAACGGCA GCTTTCAGAA AGGGAGCAGC AATTGGTGGA	480
GAAATCAGGT GAGCTGTTGG CCCTCAGCT CGAG	514

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

GAATTCGGCC TTCTGGCCTA GGA CTCTATA GAACCCACTG CCTCCTGATG AAGTCCCTAC	60
TGTTACCCT TGCAAGTTTT ATGCTCCTGG CCAATTGGT CTCAGGTAAT TGGTATGTGA	120
AAAAGTGTCT AAACGACGTT GGAATTTGCA AGAAGAAGTG CAAACCTGAA GAGATGCATG	180
TAAAGAATGG TTGGGCAATG TGCGGCAAAC AAAGGGACTG CTGTGTTCCA GCTGACAGAC	240
GTGCTAATTA TCCTGTTTTT TGTGTCCAGA CAAAGACTAC AAGAAATTCA ACAGTAACAG	300
CAACAACAGC AACAACAAC TTGATGATGA CTACTGCTTC GATGTCTTCG ATGGCTCCTA	360
CCCGTTTCTC CCACTGGTTG AACATTCCAG CCTCTGTCTC CTGCTCTAGG ATCCCCACGC	420
TCGAG	425

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs



(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

GAATTCGGCC TTCATGGCCT ACAAAGGAA AGAAGAAAAA GGGCCAAAAG CCAAATGAA	60
ACTGATGGTA CTGTGTTTCA CCATTGGGCT AACTTTGCTG CTAGGAGTTC AAGCCATGCC	120
TGCAAATCGC CTCTCTTGCT ACAGAAAGAT ACTAAAAGAT CACAACTGTC ACAACCTTCC	180
GGAAGGAGTA GCTGACCTGA CACAGATTGA TGTCAATGTC CAGGATCATT TCTGGGATGG	240
GAAAGGATGT GAGATGATCT GTTACTGCAA CTTTCAGCGAA TTGCTCTGCT GCCCAAAGA	300
CGTTTTCTTT GGACCAAAGA TCTCTTCGT GATTCCTTGC AACAATCTCG AG	352

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

GAATTCGGCC TTCATGGCCT ACACAATGGT GTTCGCATTT TGGAAGGTCT TTCTGATCCT	60
AAGCTGCCTT GCAGGTCAGG TTAGTGTGGT GCAAGTGACC ATCCCAGACG GTTTCGTGAA	120
CGTGACTGTT GGATCTAATG TCACTCTCAT CTGCATCTAC ACCACCACTG TGGCCTCCCG	180
AGAACAGCTT TCCATCCAGT GGTCTTTCTT CCATAAGAAG GAGATGGAGC CAATTTCTAT	240
TTACTTTTCT CAAGGTGGAC AAGCTGTAGC CATCGGGCAA TTAAAGATC GAATTACAGG	300
GTCCAACGAT CCAGGTAATG CATCTATCAC TATCTCGCAT ATGCAGCCAG CAGACAGTGG	360
AATTTACATC TGCATGTTA ACAACCCCCC AAGACTCGAG	400

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 278 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

GAATTCGGCC AAAGAGGCCT AAGAGATTCA GGACCTGCAG AGTCGCCAGA AGCATGAAAT	60
TGAATCTTTG TATACTAAAC TGGGCAAGGT TCCCCCTGCT GTCATTATTC CCCAGCTGC	120
TCCTCTGTCT GGGAGAAGAA GGAGACCCAC TAAAGCAAA GGCAGCAAGT CTAGTCGCAG	180
CAGCTCATTG GGCAATAAAA GCCCACAGCT TTCAGGCAAC CTGTCTGGTC AGAGTGGAA	240
TTCACTCTTA CACCCCAAC AGACCCTCCA CAGTCGAG	278

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

GAATTCGGCC TTCATGGCCT AGTTTATATA CTTTCTCTGA AGGATCCTAA TGATAGTTAA	60
CCATTTCTCA TTTTATTTT GCTGGATTGT TTTCTGTTT TGCTTCAGC ATTCTTGCTT	120
TTGCTGTGCT TACTTTTGGA GTTTGTATTC CCTGTGTCAC TGTTTTCTTT CGCATCCACC	180
ACTCGAG	187

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

GAATTCGGCC TTCATGGCCT ACTTCTCTGG AAAGGTCAC GATTGTTTGT TTTTTCGAGA	60
CAGGGTCTCG CTCTTCACCC AGACTGCAAT GCAGTGGCAC AATCATAGCT TATTGCAACC	120
TCAAACCTCGT GGGCTCAAGC AATGCTCGCT CCTCCCAAGT AGCTAGGACC ACAGGCATGC	180
ACCACGATGC CCACCTAGTT TTTTGTATTT TCTATAGAGA NGGGGGTCTC ACTGTGTTTC	240
TCAAGCTGGT CACATACTCT TGGCCTCAGG CAGTTCTCCC ACATCAGANT CTCAAAGCAC	300
TGGGCTTACA GCTGNGAGCC NGNCCTTTTT AAAAAAAAAA AAAAAATCAA AACAAAACAA	360
AACAAGATTA TGTCTTTCCC ACGCATCTCG AG	392

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

GAATTCGGCC TTCATGGCCT ACTTGGGAAT TAACATCTTC GATAAATCCC AGAAGTCTTT	60
AAGTGACAGT AGAGAGCCTA CAGAGAAGCC TGGGAAAGCA GAAAAATCTA AGAGCCCAGA	120
AAAAGTGTC TCGTCTCTCA ACTCCTCCTC CAACAAGGAA TCAAAAGTAA ACAATGAGAA	180
GTTTCGTACT AAGAGCCCCA AGCCTGCCGA AAGCCCCCAG TCAGCCACTA AGCAGTTGGA	240
TCAGCCCACT GCTGCTTATG AGTATTATGA TGCTGGCAAT CACTGGTGCA AAGACTGCAA	300
CACCATCTGT GGGACTCGAG	320

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

GAATTCGGCC TTCATGGCCT AATCAGAAGC TTTTCAAAAT TCCGTCTTCA AGAAGAAACA	60
CCCGTGGAGG AAGAAGACAT TATACAAAAC AAATTTAGAA ACTGGGATCA TGAGTGGAAC	120
AACAAAGGCA AGAAGGGCTG CCATGTTTTT TAGACGTTGC TCTGAAGACG CCAGCGGTAG	180
CGCCAGTGGC AATGCTTTGT TATCAGAGGA CGAAAATCCT GATGCGAATG GGGTAACTCG	240
ATCATGGAAG ATTATTCTAA GTACAATGCT TACACTGACT TTTCTTCTTG TAGGACTCCT	300
AAATCATCAG TGGCTTAAAG AAACAGATGT TCCTCAGAAA TCCAGACAAT TATATGCCAT	360
GCTCGAG	367

## (2) INFORMATION FOR SEQ ID NO:255:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

GAATTCGGCC TTCATGGCCT AAAGTAGTTC TGTTATAAAA AGCCAGGAAT CCTAAAACCA	60
AAATATTAGA ACGAAAACAG AAACATGGCT CACTATATTA CATTTCTCTG CATGGTTTTG	120
GTGCTGCTTC TTCAGAATTC TGTGTTAGCT GAAGATGGGG AAGTAAGATC AAGTTGTCGT	180
ACTGCTCCGA CAGATTTAGT TTTTCATCTTA GATGGCTCTA ATTGTGTTGG CCCAGAAAAC	240
TTTGAAATAG TGAAAAAGTG GCTTGTCAT ATCACAAAAA ACTTTGACAT AGGGCCGAAG	300
TTTATTCAAG TTGGAGTGGT TCAATATAGT GACTACCCTG TGCTGGAGAT TCCTCTCGGA	360
AGCTATGATT CAGGAGAACA TTTGACGGCA GCAGTGGAAT CCATACTCTA CTTAGGAGGA	420
AACACAAAGA CAGGAAGAA CCTCGAG	447

## (2) INFORMATION FOR SEQ ID NO:256:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

GAATTCGGCC TTCATGGCCT AAATGAAGCA AAATTCCATA CATCATTTTG AAAATAGTGT	60
TTCTTTCCCT GATAGGCCTG TTCTGCATCA TTCTTTTAGC TTCCTTCTGC CCTGTTTATC	120
ACTTGGTCCC ACTTTTATAT TTTTCTCTT CGTCCAGAA TTTCTATTT AGTTTCTGT	180
ATTTTGCTTA CTCCCTCCCT TCTCCATGAT TCAGCCTAGT CTTTCCGTCC TCTGTGGACT	240
TGGGTGTGCC TTCCTCTGGG CCACCTCGTC TTTTGCTGCT GTTAGCCCTC CCGCCTGCGC	300
ACCTGCCACT TCACCCTCGC CTGTGGTCCA CTTACGTTCC ACTCAGCCCG GTCAGTCCTG	360
CTTTGTTCTT CTCCACCGCC TAGGTCTCGA G	391

## (2) INFORMATION FOR SEQ ID NO:257:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

GAATTTAAGT TCCAGTATGA GATCTTCAAA GCTGTCTTTT TTTTCTTC TTCCGTTCTC	60
AGATCCTGAG	70

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

GAATTCGGCC AAAGAGGCCT AGTCAAATTC TTACCTCGCT CTTTCACTGC TAGTAAGATC	60
AGATTGCGTT TCTTTCAGTT ACTCTTCAAT CGCCAGTTTC TTGATCTGCT TCTAAAAGAA	120
GAAGTAGAGA AGATAAATCC TGTCTTCAAT ACCTGGAAGG AAAAACAAAA TAACCTCAAC	180
TCCGTTTTGA AAAAAACATT CCAAGAACTT TCATCAGAGA TTTTACTTAG ATGATTTACA	240
CAATGAAGAA AGTACATGCA CTTTGGGCTT CTGTATGCCT GCTGCTTAAT CTTGCCCTG	300
CCCCTCTTAA TGCTGATTCT GAGGAAGATG AAGAACACAC AATTATCACA GATACACTCG	360
AG	362

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

GAATTCTAGA CCTGCCTCGA GTGCGGATCC AGCCGGAGGC GAAGAGAAGC ACTTTGGGGG	60
CAAAAGAAGA GAAAAATGAA GACGGGACAT TTTGAAATAG TCACCATGCT GCTGGCAACC	120
ATGATTCTAG TGGACATTTT CCAGGTGAAG GCTGAAGTGT TAGACATGGC AGATAATGCA	180
TTTGATGATG AATACCTGAA ATGTACGGAC AGGATGGAAA TTAAATACGT TCCCCAACTG	240
CTAAAGGAGG AAAAAGCAAG CCACCAGCAA TTAGATACTG TGTGGGAAAA TGCAAAAGCC	300
AAATGGGCAG CCCGAAAGAC TCAAATCTTT CTCCCTATGA ATTTTAAGGA TAACCATGGA	360
ATAGCCCTGA TGGCATATAT TTCCGAAGCT CAAGAGCAAA CTCCCTTTTA CCATCTCTTC	420
AGTGAAGCTG TGAAGATGGC TGGCCAACCTC GAG	453

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

GAATTCGGCC TTATGGCCTA CTTTAAAAAA AAACCAATAC CAAAGAAGCC TACAATGTTG	60
GCCTTAGCCA AAATTCTGTT GATTTCACG TTGTTTTATT CACTTCTATC GGGGAGCCAT	120
GGAAAAGAAA ATCAAGACAT AAACACAACA CAGAACATNG CAGAAGTTTT TAAAACAATG	180
GAAAATAAAC CTATTCTTTT GGAAAGTGAA GCAAACTTAA ACTCAGATAA AGAAAATATA	240
ACCACCTCAA ATCTCAAGGC GAGTCATTCC CCTCCTTTGA ATCTACCCAA CAACAGCCAC	300
GGAATAACAG ATTTCTCCAG TAACTCATCA GCAGAGCATT CTTTGGGCAG TCTAAAACCC	360
ACATCTACCA TTTCCACAAG CCCTCCCTTG ATCCATAGCT TTGTTTCTAA AGTGCCTTGG	420
AATGCACCTA TAGCAGATGA AGATCTTTTG CCCATCTCCC TCGAG	465

## (2) INFORMATION FOR SEQ ID NO:261:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 491 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

GAATTCGGCC TTCATGGCCT AGCGGCGGGG CGAGCGCCTC CACGCAGCAA CTCCGGAGTC	60
CCCCGCTTGC CCGAGCGCAG TTTCTCCGCT GCTGTTTCCA CCGGCTTTGT AACACTGGGA	120
ATTTACATCC TCACCCGCAC CCTCAGGCC CGAGGATTTT AAACACCTT TACTCTCGA	180
ACTGAGAGTT GCGGTAGATG GGATTTTTC CTTTCCCCA GATGGTTGAA GGTTAAGATT	240
TTTGGAAACC CCCCCACCTC CTTATTTCTA TTATTATTTT TGCNAGAAAA GTATAAAGAG	300
AGTTGTAGTG GAGGTGAGAT TTGTGATCGG GAAAGCCTTC GACTCCCTCC TTCTCCGTCT	360
TCCGCTTCTC TCTCTCTGAT TAGTTCCTAT CCAGCAGCAG ATTGAAGCAG GAGATGATTC	420
TTCTCAAGGT TTGTTTCAGCA GCTTCACTTC TAGGCGAAGG CTTTCATGAAC CAAGTGACGA	480
ACAACCTCGA G	491

## (2) INFORMATION FOR SEQ ID NO:262:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 231 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

GAATTCGGCC TTCATGGCCT ACATTTTCT ATTGATATAA AAATTGTTAG AGAAATATAC	60
AGTTGTATAT TTCCCCCTT TATACAGAAA TTTTACAATA ATTTGAGATT TTTCTGAGTT	120
TTTTCAGATT TTTGATTCTA TAATATGAGA TTATCTTTC TTCCTCTTAT TTTTTAGGT	180
TATTTATTTT TTCTTTTCTT TTTAATTTGC TCATACAGGT TACTCTCGA G	231

## (2) INFORMATION FOR SEQ ID NO:263:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 445 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

GAATTCGGCC	TTTCATGGCCT	AGTAAAATTT	AAAATACATA	CTAACATATA	ACCCAATTTT	60
AACATATTAA	GTGAATATGT	ATTCTTAAAA	GATCCACTAC	TTTACATTTA	GATGCGTTAG	120
GATGTATTAG	AAATAAAAAAC	AGAAGAAAAG	ATTTAGAATC	TAGTCTGTCT	TTGCCACTCA	180
AGCTAGTTAC	CCTCTCTGAG	TTTTATACCC	CCTTCATCTA	TTAAAATGGG	GGGTAACGCC	240
AACCTGACTC	CTTTAAAATG	AGTTTGAGAG	TCAGGC AAAAT	TAGAAAAGATA	CATAGATGAA	300
AAC TTTTAA	AAAGTATATA	GTCTTTCATG	ATTTGTAGAA	CACTTTTATA	CTTTTCAGAG	360
TACTTTCACA	TTGATCATAT	TGTTTG TACT	TTATGAAAGT	CTTCTACAAA	TCAGAATTAT	420
GCTTATTATA	CAGATGTGGC	TCGAG				445

## (2) INFORMATION FOR SEQ ID NO:264:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

GAATTCGGCC	AAAGAGGCCT	AATTACTTTA	TATTTTAAAA	GCTCTGTGAC	TTCAGTAGTG	60
CATTGAAATA	AAATTTTAT	TCATTATGAG	AGAGTCTGTG	AGGAACAGAA	TCATGGTTCC	120
TGTGTGTTTG	AAGATATGGC	GTGGGGTGAT	AGTGCTGGCA	GCAGCTCTGT	TGCTCTTG TG	180
CCCATGGCAT	ACAGACTGGA	TCTGCTGGTC	CACGGCTCCT	GAGGTTAATG	TCCAAGCCCT	240
CTGCAATGCT	GACAGTCTTC	CTCATCCTCA	CACCCTACCT	CTCAGTTTCT	ACCTGCCACC	300
TCCCCAGTAA	TATTAGCCTC	TTGAGTCCCC	AACAACACTC	GAG		343

## (2) INFORMATION FOR SEQ ID NO:265:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

GAATTCGGCC	AAAGAGGCCT	ATTAAAATTC	ATTTATCAGT	AGGATCATTC	TGTTCTAGAC	60
AAGTTGGCTA	TATTATAAAA	CATTAAAGCA	GCAGGCACTA	AGTTAAATAT	TGTAGCAGTT	120
GAAATTTAAT	GCTAATCTTA	CAGTTT TACA	CAGTTAACAA	TCTAGGCCAA	ATCTATTGAT	180
ACCTTTGGAA	CTACCCTTTA	AATTCATCC	TATGCTTG TG	AAAAGGTTGC	ATATAATTTT	240
TTTTCTTTT	TCTCTCTTCT	CTTCCTCTTC	TTTTTCTTT	TTCTTTTCT	ATTTCCTTT	300
TCTTCCTTTT	TCTTTCACAG	AGTCTTG GTA	TATCACCCAC	ACTCTCGAG		349

## (2) INFORMATION FOR SEQ ID NO:266:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

GAATTCGGCC AAAGAGGCCT AGAATAAAAA TGCTTGTGTC AAAAAATCAA ACATTTGTCT	60
CTTTCCTTTC CATTCCAGTT CTAGGTCTCG TTCCAGATCA TATTCTCCAG CTCATAACAG	120
AGAAAGAAAC CACCCAAGAG TATATCAGAA TCGGGATTTC CGAGGTCACA ACAGAGGCTA	180
TAGAAGGCC TATTATTTCC GTGGGCGTAA CAGAGGCTTT TATCCATGGG GCCAATATAA	240
CCGAGGAGGC TATGGAACT ACCGCTCAA TTGGCAGAAT TACCGGCAAG CATACAGTCC	300
TCGTCGAGGC CGTTCAAGAT CCCGGCTCCC TCGAG	335

## (2) INFORMATION FOR SEQ ID NO:267:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

GAATTCGGCC AAAGAGGCCT AGTGGAAATT TGTGGCTAGT GTGATTTTGG TTTGTTTCCT	60
TTTAAGTACT GTTGATCAGT TGTGACACTT ACTGGTTAAA CTTACGTTGC TAAAGATTTC	120
TCTATAATAA GCCACACATT ATATTTAGAC TATATTAAGG GACCTTGTT TTCTTCTAGA	180
TAGCAGCTGT CCCAAAGAAA ATATTTCTTC TTTGTCTGTT AAGATTTAGC TATTATCTGC	240
CAGTTGTAA GAGGTTTGG TTCCAACTC AACCAGCAAT GTTGAGAGCT GAACTTAAGA	300
TAGCTGTTGT ACTTTTGTCT TTCCATCTGT TACTGTCCTT CATTCTTGGC TCCCTACTAT	360
CTATAAACAG CAAGCTCGAG	380

## (2) INFORMATION FOR SEQ ID NO:268:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

GAATTCGGCC AAAGAGGCCT ATCTAGACCT GCCTCGAGTC AGCAACAACA ATTTTAAAA	60
TTTCTTTCTG GATTCTAGAG TGAGTTTTTT TCATAACACA AGAGGATAAG AGTGAGGACA	120
ACAGGAGGTA TTGATGATCT GCTGAGCACC AGGCATTATG CTAAGTGCAT TCACACACAT	180
CTCAGTGCCT ATTGCCTCGT TGTGGACTTC TCTATCCCAG CTCGTCCCCC TGGCAAATTC	240
TTTCTCATCC TTCAACTCTC AGACACCTCC CCCGCGCCTC GAG	283

## (2) INFORMATION FOR SEQ ID NO:269:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

GAATTCGGCC AAAGAGGCCT AACCAGGCAT TTTTCATTAG GGTTCTAGGT CCAGGTGAAT	60
TCTTGAGTTG GTTCGTTGTG TCATGTATTG GCCTTAATA ATGCTCTTAT TTTGGCCAC	120

GCCTGTGGTC CCAGCACTTT GGGAGGCTGG TCTCGAG

157

## (2) INFORMATION FOR SEQ ID NO:270:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

GAATTCGGCC AAAGAGGCCT AACCAGGCAT TTTCATTAG GGTTCAGGT CCAGGTGAAT 60  
 TCTTGAGTTG GTTCGTTGTG TCATGTATTG GCCTTTAATA ATGCTCTTAT TTGGGCCAC 120  
 GCCTGTGGTC CCAGCACTTT GGGAGGCTGG TCTCGAG 157

## (2) INFORMATION FOR SEQ ID NO:271:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

GAATTCGGCC AAAGAGGCCT ACCCAAATAA AATCAGAGTC AGAAATGGAA ACAGACAGTG 60  
 GAGTACCTCA AAACACTGGA ATGAAAAATG AAAAAACAGC CAACAGGGAA GAGTGTGCA 120  
 CCCAGGAGAA AGTTAATGCA ACAGGACCAC AGTTCGTGAG TGGAGTGATT GTGAAGATCA 180  
 TTAGCACAGA GCCTCTACCT GGCAGGAAAC AAGTCCGGA TACTTTGGCA GCAATCTCAG 240  
 AAGTTCTTTA TGTTGATTG CTAGAAGGGG ATACAGAATG CCATGCTAGA TTTAAACTC 300  
 CTGAGGATGC TCAAGCAGTA ATAAATGCCT ATACAGAAAT TAACAAGAAA CACTGCTGGA 360  
 AACTCGAG 368

## (2) INFORMATION FOR SEQ ID NO:272:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

GAATTCGGCC AAAGAGGCCT ACAACGAACG GCTTGGGNGC GGACTGGTAT CCGGGGACTG 60  
 TGACTTGCA GGTCCGCCAT GGAGCCAGAG CAGATGCTGG AGGGACAAAC GCAGGTTGCA 120  
 GAAAATCTC ACTCTGAGTA CGGTCTACA GACAACGTG AGAGAATAGT AGAAAATGAG 180  
 AAGATTAATG CAGAAAAGTC ATCAAAGCAG ANGGTAGATC TCCAGTCTTT GCCAACTCGT 240  
 GCCTACCTGG ATCAGACACT TGTGCCTATC TNATNACAGG GACTTGCTGT GCTTGCCAAG 300  
 GANAGACCAC CACATCCCAT TGAATTCTA GCATCTTATC TTTTAAAAA CAAGGCACAG 360  
 ACTCGAG 367

## (2) INFORMATION FOR SEQ ID NO:273:



- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 250 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

```
GAATTTGGGT CCTAGGATAT AAATATTTT CCCTTTATAA GATATTTATA GGATATTGCA    60
AACAATTCT GTTTTTCAT ATCCTTGCCA GCAGTTAGGG TTATCAAATT CTTTGATTTC    120
TTACTGATT GTAAGTTTT TTGTTTGT TTAGGTATT TCAGGATAGT TACAAATGTT    180
AGGAAACTT ATTTTATTT GGCTTTTGAA GTTCCAGAT TTCTGAACA GTGACCAATA    240
TGGACTCGAG                                         250
```

(2) INFORMATION FOR SEQ ID NO:274:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 133 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

```
GAATTCGGCC AAAGAGGCCT ATCTTTTTC CTCTTTTTT GTTGCGAGAA TGATAACCTA    60
CTATTCAC TA TTCTGTGCCT TGCTTTGTTT GCATACTGAA AATTATCCAT GGAAGGATAC    120
AGCACCACTC GAG                                         133
```

(2) INFORMATION FOR SEQ ID NO:275:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 396 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

```
GAATTCGGCC AAAGAGGCCT AATGAAACAT TTCTGTAACC TGCTTTGTAT CTTGATGTTT    60
TGTAATCAGC AAAGTGTATG TGACCCGCCT TCACAAAATA ATGCAGCAAA TATTCCATG    120
GTTCAAGCTG CTTGAGCAGG ACCCCATCT CTGAGAAAAG ATTCGACTCC AGTTATAGCC    180
AATGTAGTAT CATTGGCAAG TGCCCTGCT GCTCAGCCTA CAGTGAATTC TAACAGTGTC    240
TTACAAGGTG CAGTTCCAAC AGTAACAGCG AAAATCATCG GTGATGCAAG TACTCAAACA    300
GATGCCCTGA AACTGCCACC TTCCAACCT CCAAGGCTTT TGAAGAACAA AGCTTTATTA    360
TGCAAACCCA TCACACAGAC TAAAGCCACA CTCGAG                                         396
```

(2) INFORMATION FOR SEQ ID NO:276:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 391 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

```
GAATTCGGCC AAAGAGGCCT ACCCCTCCCC ATTTCTAGTT TCATGAACTG TGCACAGGGA      60
TATGGGGCTG TTCGAGGTAC TTTTGGGCTG ACCAAGGCTC AGAGGCTACT GACAGCTTTG      120
CTGCAAGTAA CTTCTAGGCC TTGTGGGTCC CAGTGCAGGG AACCCATGTG CGGTGACACT      180
GGAGAAGCCA TCTGATCCAG GTCTCTCACT TGACAGATGG GGAAACTGAG GTCCAAAGAG      240
GTACAGCAGC TTGGTTTAAG AGATAGAGAT GGAAC TGGA CAAAAATAAT AACCATTTGA      300
TAATATTTTA ACATTTATTG ATTTGTTTTT ATATGCCAAG ACCTTTTAAA GCATTATCTC      360
CTTTAAACTC TCATAACCAC TCTTACTCGA G                                     391
```

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

```
GAATTCGGCC AAAGAGGCCT ACTGCTTCCT GATCATTGT CTTTTTAAAT AAAAATATGA      60
TATTTGAGAT TCTTTTATTC TCTTTAAATA TTTGAATACA GAGTCTATTT GAAGGACCAG      120
TATATTGAAT AGCAGTAATA TTTGAAGGAC TAGTCAGCTG TAGAAGCCTT GACTTCAGAT      180
CTTCACCCAA GAAACTCTGT GTATTTGCTT TTCCTGGGCC ACTCAGATAG ACAATTGTGT      240
TTTGATACA GTAAGAGTTT GCAGCTTAGC TTAAC TAGAA ATAATCCGGA TGCTCGAG      299
```

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

```
GAATTCGGCC AAAGAGGCCT ACTAGGATTT GAGGAGGACG CCTCTTTTGC AGGAGGATGC      60
AGTGAACAGC CAAAGTCATC TGACATCCTT TTCCATCTTT TTCCTTCTAG TATCCCAGTT      120
TCAAGGCCCA GGAAAGGCAG GACTAACAT ATGGAGCAGT TACCCAGAG TTCAAAGGGT      180
TAATCTCTAA GAATTCATTC TCTGACACCA GCCACAGCTC TTGTCCCCAT CTCTGGGACC      240
GTCCCCCTCT AGCCCCAGGT TGGCAGCTTC CCTGAATGCC TTCTATGATA TAATTGTGTA      300
TTCGGCAGGG CTCTGGGACC CAGGCTCAGA GACCCAGGCT CTGCTCTCTC CTCAGTTTCC      360
AGGAGTCAGG GCTTGCTCTA AGGGAGGAAG TAAACAGGCC TTTCCCTTGC TCCCTCTCCT      420
TTTCCTCGAG                                     430
```

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

GAATTCGGCC	AAAGAGGCCT	AGTGGGAGTT	AGATGTATTA	TATAAAAATG	TCCCCAGCAT	60
CAAAATGACT	CAGAGTATGA	CTGTATTTTT	AAATTAAATA	TCAAGACCTA	TCATCTGACA	120
AAACATATGA	ATGACAATGA	GATATAATAT	TTGAAATTAG	ATCCGTTCTG	GGGAATCAAA	180
GATATTTTGT	AACAGTATAC	ACAGTAGGCA	TTGGTAAGTA	AATGAGAACT	CTATGAGCTG	240
TTTTCTGGAA	AAGTTTAAAA	TGAAATTTGT	CAAATATCAA	ATGATTGTTA	TAAGAAAATC	300
AGTGGAGGCA	GTATCCTTGG	AAAAATCCAG	AAACAGTTTT	GTNTGTTTGT	TGTTTTTTAC	360
ATCAAGGCAG	ATCAGCAGGT	GAACAGCTCG	AG			392

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

GAATTCGGCC	AAAGAGGCCT	AGAAGAAACT	TTTTCTTGGG	AGCAAGGTAG	TTATTTCAAA	60
GCACAGAAAA	AGCGGCGGG	GGGCACAGAG	AAGCACAGAG	AAGCGGGGGC	AGTTGCTCAG	120
GTAAAACATT	CATCTTGGCT	TTTCTTTTTA	AAAGATAAAC	TTTGTCACAC	GTAAAGAGGA	180
AAACTGCATA	GATATTCATT	GAGATTATCT	GATTTGTAC	TGTTGCCAAA	GAAAAAACAA	240
AGGTAAATA	CACGAGTTTC	TGCATTGAGA	AGAAAGTATT	TCAGGTAAAA	ATTAACATT	300
AAGCAACTTT	TCTCAGCAGA	AGAAATGCCC	AAATCTTAA	GGACAGTACT	CGAG	354

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

GAATTCGGCC	AAAGAGGCCT	ACTTTGAGAT	TTTTTTGTTG	TTGTTTCCTT	TTGTATTTT	60
ACTGATATCA	CCAGGATAGT	TTACTCTCCT	TCTAGCTTTC	TGCTTACCGC	ACACTGGATG	120
ACACACACAT	ACACACCCGC	AAAAATGCTC	ATGAACCCAA	TCCGGAGAAG	GTTCCAGCAG	180
GTCCCCCACC	CTCCCCCTCT	CGTCCTACTT	CTCCTCTTGA	CAGCGAGGAC	AGGAGGGGGA	240
CAAGGGGACA	CCTGGGCAGA	CCCGCCGGGT	CTCCCCCACC	CCCACCCGGC	CCTCANATCA	300
TACTCGAG						308

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

GAATTCGGCC AAAGAGGCCT AGACCTGCCT TGTGTTTTCC ACCCTGAAAG AATGTTGTGG	60
CTGCTCTTTT TTCTGGTGAC TGCCATTTCAT GCTGAACCTCT GTCAACCAGG TGCAGAAAAT	120
GCTTTTAAAG TGAGACTTAG TATCAGAACA GCTCTGGGAG ATAAAGCATA TGCCTGGGAT	180
ACCAATGAAG AATACCTCTT CAAAGCGATG GTAGCTTTCT CCATGAGAAA AGTTCCTAAC	240
AGAGAAGCAA CAGAAATTTC CCATGCTCTA CTTTGCAATG TAACCCAGAG GGTATCATTC	300
TGGTTTGTGG TTACAGACCC TTCANAAAAT CACACCTTTC CTGCTGTTGA GGTGCAATCA	360
GCCATAAGAA TGAACAAGAA CCGGATCAAC AATGCCTTCT TGTAAANGA CCAAACCTCTG	420
GAATTTTAN AAATCCCTTC CACACTTGCA CCACATCTCG AG	462

## (2) INFORMATION FOR SEQ ID NO:283:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

GAATTCGGCC AAAGAGGCCT AGCAGATTCT TAATTTCCCT GTCCATATTT TCCCCTTTCC	60
TTTCTCCCTG CCCGTTCCAT GGTCTTATCT GGCTGCTTTC TCAATTTATT CTTGGTTGCT	120
TGTGGATTCC CTTCTATTAA TCTTGAAGTC GTTACTGACA TGTTTGGCCC TATACCAGCT	180
AGACCATTGC CTGAAGACTT TTTGATGAAC AATCTGTGTA AAGAAAAGG GAATCTCGAG	240

## (2) INFORMATION FOR SEQ ID NO:284:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

GAATTCGGCC AAAGAGGCNT ACCAGGANTT TCTATTCAAT TGAGAAGAAC CCAGCAAAAT	60
GGGGATCTCC ACAGTCATCC TTGAAATGTG TCTTTTATGG GGACAAGTTC TATCTACAGG	120
TGGGTGGATC CCAAGGACTA CAGACTACGC TTCACTGATT CCCTCGGAGG TGCCCTTGGA	180
TACAACGTGA GCAGAAGGTT CTCCATTTC CTGAGAGTTG ACCCTGGAGT CAACTGTAGC	240
AGAAGGTTCT CCGATTTCCT TGGAGTCAAC CCTGGAGTCA ACTGTAGCAG AAGGTTCTCT	300
GATTCCCTCA GAGTCAACCC TGGAGTCAAC TGTAGCAGAA GGAATCCGAG	349

## (2) INFORMATION FOR SEQ ID NO:285:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

GAATTCGGCC AAAGAGGCCT AAAAAAATAA GAAATAATCT ATTCCACATT TAATAATTTG	60
AATCTTCCTG CTATAGATAT TTGGTTATCT TGACTIONTTA ANATAACATA TTTCTACAGG	120
ATTTTGAGTC TGAGAAGAGA AAGGTAANAT GCAAGACACT TCGATTTGTT GCACATTATT	180
ATGGAGCATC ATTAATGGTT TGNACATTTC TTGTCCTTTG GGCTTGAATG GACAGTACCA	240
AATTTGGGGT AATCAGCAAC TTGATGCACA GCTACGAGGA ATAAATGCTT TTGCTAATGC	300
ACTCGAG	307

## (2) INFORMATION FOR SEQ ID NO:286:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

GAATTCGGCC AAAGAGGCCT AAAAGATTAA AAAAAAATTT GTGTGATTTG ACTATATATT	60
AAAATCTCTT TCATAATTAG TCAACAATTT AAGCAACAAT TAAATTATTA GTGCTGTGGA	120
AAATATAGAA GAAAGATAAT TTCTTATCC CCTCCTGAGG AAAGCATTG ATACACCTGG	180
AAAGGAGCTG CTATGAAGCC AATTTATCTG TTCTTTTAT CAATTCAGCA GCATTTAAGA	240
TCAGATTTT TCTCTAGTGG TCCAGCAGAG GGAGCCCTAG CACATGAATT GTTTTCATTT	300
CGTGCTTGCA CCCAGGATCT CGAG	324

## (2) INFORMATION FOR SEQ ID NO:287:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

GAATTCGGCC AAAGAGGCCT AAGAGAGATC AGTAAACCA CTGGNAAAGA AAAGATGGAG	60
AAAATGTTGG AAAACCAGAA CTGTNTGCTG TCAAGNTCAT GTGGAATGTT CAAGAAAGAA	120
TCTGACTCTA TTATCTAATA TCTTACATAC NTCCACCAGA CTGGACTTGC TATTTGAATT	180
TTAAGCAAGT TTCTTTTCT TTTATACAAA TTGCAAATTT CATATTTTTA TAATCACATC	240
CTAGGAATAG CACAATAATT GGGAAATAGA ACCCTTATCA CTAGNAGAAC CATTTTCCTG	300
CCACTCTCGA G	311

## (2) INFORMATION FOR SEQ ID NO:288:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

GAATTCGGCC AAAGAGGCCT ATGCCCCATA AAAGGGCTCC TGAAGCTCTT TGTGAAGGGG	60
TCTGAAAAGG GCAGATCAGG GTGTCCTTTG GGGCGGATGT GGGGTTTGGG ACAATTGCAT	120

GTGATTGTCA TTCTTTAGCT GTCTGCATCC CACAGAACT TTTTCTGAG TCTCCAGCT	180
GGCCCAAGTC CTGGGTCTCT TTTACTGTTT TTGTAGCTGA CTACAGTAGG CAGATGAGGA	240
ACTCTTAGTC AATCTGGAAA AACTCGACTG ACTATAAACA ATCCTAAATT GAAAGAAAGG	300
TCTCGAG	307

## (2) INFORMATION FOR SEQ ID NO:289:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

GAATTCGGCC AAAGAGGCCT AGCCGGTGTG GGGAGGATTG GCTCAGCCAC CCGCTGGGAA	60
TCGTGCAGGG ATTCTTCGCC CAAAATGGAG TTAATCCTGA CTGGGAGAAG AAAGTAATTG	120
AGTATTTTAA GGAAAAGCTG AAGGAAAATA ATGCTCCTAA GTGGGTACCA TCACTGAACG	180
AAGTTCCCTC TCATTATTTG AAACCTAATA GTTTTGTGAA ATTCGTTGC ATGATTCAGG	240
ATATGTTTGA CCTGAGTTT TACATGGGAG TTTATGAAAC GGTTAACCAA AACACAAAAG	300
CACATGTTCT TCATTTTGA AAATATAGAG ATGTAGCAGA GTGTGGGCCT CAACAAGAAC	360
TTGATTTAAA CTCTCCACGA AATACCACTT TGGAAAGACA GACTTCTAT TGTGTTCCGG	420
TGCCTGGGGA ATCTACGTGG GTAAAGAAG CCTATGTTAA TGCAAACCAA GCTCGAG	477

## (2) INFORMATION FOR SEQ ID NO:290:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

GAATTCGGCC AAAGAGGCCT AAAAAATCT TCTGGAAATA ATTCTTAGCT GTGTAAGAAA	60
TTTGATACTT AAGGAGACAG CAGTGGAGTC ACTTAACTAA TTTGTGTGG TTTTGACCT	120
GCATAGTGAC TGCCATTAC TTTATGTTT TGGTCAATTA GATACTAAGT AAAAAGATAG	180
TTGGTATTTT GGCTTCAGAT CAGGTCTATT TCTCCAATT CTATATATCC TTTCTGTGAT	240
TAAACAAAT AAACAATCCT CAGTATCATC ATTTAACACC TCTAACTGAT AGAAAAATG	300
AGGTTGTGGG TCCTCGAG	318

## (2) INFORMATION FOR SEQ ID NO:291:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

GAATTCGGCC AAAGAGGCCT AACCTGGGA TTTTCTATAT ATATGATGGT CTCATTTGTG	60
NATAACACA ATTTTATTTT TTCCTTTCCA ATCTGGATGC TTTTTTTTTT TNCCTATTGC	120

ACTGCCTATT GCATTCCTAA AACTCCATT CCAATGTTCA ATAGAAATGG TGAAAGTGA 180  
CATTGGAATG GAGTTTTTAG GAATGCACTC GAG 213

## (2) INFORMATION FOR SEQ ID NO:292:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 644 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

GAATTCGGCC AAAGAGGCCT AAAAAGAATT AACCAGCTCT TCAGTCAAGC AAATCCTCTA 60  
 CTCACCATGC TTCCTCCTGC CATTCAATTC TATCTCCTTC CCCTTGCATG CATCCTAATG 120  
 AAAAGCTGTT TGGCTTTTAA AAATGATGCC ACAGAAATCC TTTATTCACA TGTGGTTAAA 180  
 CCTGTTCCAG CACACCCCAG CAGCAACAGN ACGTTGAATC AAGCCAGAAA TGGTTGCAGG 240  
 CATTTCAGTA AACTGGACT GGATCGGAAC ACTCGGGTTC AAGTGGGTTG CCGGGAANKG 300  
 CGNTCCCACC AAATACATCT CTGATGGCCA GTGCACCAGC ATCAGCCNTA NGAAGGAGNT 360  
 GGTGTGTGCT GCGAGTGAC TTGCCCTGC CAGTGCTCCN TAATTGGNTT GGAGGAGGCT 420  
 GTGGAACAAAN GTANTGGAGC AGGAGGAGCT CCCAGGNGTG GCGGTGTGTC AATGACAAAA 480  
 CCNGTACCCA GAGAATCCAG NTGCAGTTCC AAGATGGCNG CACACGCACG TACAAAATCA 540  
 CAGTAGTCGG TGCCNGCAAG TGCAAGAGGT ACACCCGGCA GCACANNAG TCCAGTCACG 600  
 ANTTTGAGAG CATNTCACGT GCCAAGCCAG TCCAGCAACT CGAG 644

## (2) INFORMATION FOR SEQ ID NO:293:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 299 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

GAATTCGGCC AAAGAGGCCT ATTTNTGGAT GGTGCTAGCG AANTAGAGGC TAATCCCCAA 60  
 CATGAGGTTT TTCTAATTT ANGGTGTGA TTTCCAGTG AAAGAAATNA ANAAGAATTT 120  
 GCAGATTCGT GGAGACTTGG GAAGGATATN AAGCTGTCTT ACAACCCCAG ATTCACCCAA 180  
 AATTCAGCAA ATCACTGAAT ATTCNNAATA AAAATTGAAG TATTTTCNAA CTCAGTTT 240  
 TATCTCCAGA GGTNACGTC CNATGTAATC CGAAATCCTC ACGANGACAT AACCTCGAG 299

## (2) INFORMATION FOR SEQ ID NO:294:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 310 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

GAATTCGGCC AAAGAGGCCT ACAACAACAA CAAAAGAAGA ATACTAATTA GAATTTGAGT 60  
 TCTAGGGGTT TTCCTAGGT TTTTCATTCT AGACTTAGCT TTTATTCAA CCTGTTGATC 120

CTGCATAGGG GTAGTCTAGC TTAAAAAAT AAAACAATAA ACATAAATGA GCCTATTGAG	180
TTCAATCAGA GTAGGGAGCA GTTTTATTGA ACAGCACATT TTCAAATCT TCAGTTGTGT	240
TTTGTTTTTC AGCTACGTGT CTCTCTGTGA TAATGAAAAG ACAGGTTGCA AAGCCCGGGA	300
TTCGCTCGAG	310

## (2) INFORMATION FOR SEQ ID NO:295:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

GAATTCGGCC AAAGAGGCCT ACATCTATTG AGGAAAACCA CAAAAAATT CAAAACAGCT	60
ACAACGGGAA AAAGAGAGTT TTGTCCACCA GTCAGCAGGC CACTAGTTTA TTAACCTCCA	120
GTCACCTTGA TTTTGTCTAA AATGAAGACT CTGCAGTCTA CACTTCTCCT GTTACTGCTT	180
GTGCCTCTGA TAAAGCCAGC ACCACCAACC CAGCAGGACT CACGCATTAT CTATGATTAT	240
GGAACAGATA ATTTTGAAGA ATCCATATTT AGCCAAGATT ATGAGGATAA ATACCTGGAT	300
GGAAAAAATA TTAAGGAAAA AGAACTGTG ATAATACCCA ATGAGCTCGA G	351

## (2) INFORMATION FOR SEQ ID NO:296:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

GAATTCGGCC AAAGAGGCCT AGAGTGAGAC CTTATCTTAA AAAAAAAAAA AAAAAAATTG	60
TCTATGATTT TTTTAAAGC TTTTATTTT GAACATAATT TAGACTTGCT TAAAGTTGC	120
AAAAATAAGA CACAAGTTTC ATATATCACT CAATCTGCTT CCTGTAATAT TAACAACATA	180
AATAGCCACA GGGAAATCTT CAAGACCTGG AAATTAAC TGAGACAGCA CTATTACCTA	240
AACCACAGCT CTAATTTGAA TTTTCATCAGT TTTTCTCCTA ATGCTGATT TCTGTTCCAG	300
GATCCTATCC AGGAGCCAC ATTGCTCGAG	330

## (2) INFORMATION FOR SEQ ID NO:297:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

GAATTCGGCC AAAGAGGCCT AAAAAAATAT AAGTAACAGA GGNAGAAATA ACTGTTATT	60
GTCAAGTGAC AAGCTTTTAA TGTCAGAATG GCTCACCTAA AGCGACTAGT AAAANTACAC	120
ATTAAAAGAC ATTACCATAA AAAGTTCTGG NAGCTTGGTG CAGTAATTTT TTTCTTTATA	180
ATAGTTTTTG TTTTAATGCA AAGAGAAGTA AGTGTTCAAT ATTCCAAAGA GGAATCAAG	240



ATGGAAGGG ACATGAAAA CCAAAACAAG ATGTTGGATT TAATGCTAGA AGCTGTAAAC	300
AATATTAAGG ATGCCATGCC AAAAATGCAA ATAGGAGNCA CCTGTCAGGC AAAACATTGA	360
TGCTGGTGAG AGACCTTGTG TGCAAGGATA TTATACAGCA GCAGAATTGA AGCCTGTCCT	420
TGACCGTCCA CGTCTCGAG	439

## (2) INFORMATION FOR SEQ ID NO:298:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

GAATTCGGCC AAAGAGGCCT AATTATTTCT TGTCTCTCCC CAAATGAAAT CTGGGACATT	60
ATGACAATTT ATTTTCTAA GGATGATCTT GGTCTGCCT ATTGAAATGT CCTCACTCAC	120
CTCCAAGAGG AAGGGGGATG GCTTCAGAAA ATGTCTTTAA GTGTTTTTAT TTTTCAGGAG	180
TTATTTATTG CAACACTAGC TCTTCCCTGC AGGAAGCTAT ATAATTGTGT GCTTAATTGC	240
TAACATAGAA GAATTCCTAG CTACTTCCTA GAGAATATAC TGTGAATTC CTTGTCCTC	300
AAGTATCTGT TAAAACTCA ACCGTGGGAA ACAATGTCTA TGGATGCCTT TGGGAAAATA	360
CACATTTTAC CTATTATTTT ATCTTTTTC TCACTTTGTC AAGTAGTAGG TACCCCACTG	420
TACTCGAG	428

## (2) INFORMATION FOR SEQ ID NO:299:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

GAATTCGGCC AAAGAGGCCT AACATTATCG ATTCCATTTT TTTACTGTTG TAATTCTGCT	60
TCTTATTGCC TGTGTAAATT TCTGCTCTAT ATTAGTTTCC TGATACCCCTA TCATTAATTC	120
AGTCTGCCCT TTTTCATAT CATTCTACTG TTTGTCTCA TCTTCCTTAT ACTTTATTCA	180
GAGACTGTGT TTTTCATGAAG TTTGTGAAAA ACATTTTAAA AATTGTTTAA AATGTACTCT	240
TTGTCTATTT CTTGCTATTT TTTCTTTTGT ATATTCTGGA ATATATCCAC AGCGCTCGAG	300

## (2) INFORMATION FOR SEQ ID NO:300:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

GAATTCGGCC AAAGAGGCCT ATAGATTGTT ACATTTGTTT TGTGCATTCC ATGAAGTTTC	60
TTACCCCTTAG AGTTATTTCT GTCTTAGTAA CAGCAACAAG TGGGAATGGA GACTTTGGTG	120
ACTGGAGTGC CTTCAACCAA GCCCCATCAG GCCCTGTTGC TTCCAGTGGC GAGTTCCTTG	180

GCAGTGCCTC ACAGCCAGCG GTAGAACTTG TTAGTGGCTC ACAATCAGCT CTAGGCCCCAC	240
CTCCTGCTGC CTCAAATTCT TCAGACCTGT TTGATCTTAT GGGCTCGTCC CAGGCAACCA	300
TGACACTCGA G	311

## (2) INFORMATION FOR SEQ ID NO:301:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

GAATTCGGCC AAAGAGGCCT AGCGCGGTGT GTCGTGGTGT GGCGCGGTGT GGCATGGCGT	60
GGTGTCCTCAG CTGCTACAC ATTTGTGGTT TTTAAATGTT TGTGGATAC AGTAACACTT	120
TGTTAATTTT AATTATATGC AAGATAACTT GATTGCCCTA AAACAGCCAT TTGGGTCAAG	180
ATAAAGCCAT CGCCCTCTGA AGGGGCTGA GCTGGGTGTC TCCTCCATCA GTCGNTGTGA	240
TAACTCTATG CCAGTTTCGA TTTCCAAAGT CAGAAGTGCA AAGCAGGGCT GGTATTATAT	300
CNTGTCAAAT CGTCCAGGTC CTGTGTNGTC GNACTCCATT ANTTATNTAG GTCCATANGA	360
TGTGTCTTAC NACGNAACAA ACCCTCTCTG AG	392

## (2) INFORMATION FOR SEQ ID NO:302:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

GAATTCGGCC TTCATGGCCT AATGGAATTT GAGTCCAAAG GTAAATATAT TAAACATATA	60
GATAAGAAGA AAAGAAAAAC GTTATTTAAG TATCTGATCA GCTCTGCACC CCAGGGACCT	120
CCACTTTTGC CCAGGTTTGA GAATTTGATC TATAGAATTA CCTGCATTCT TTCCCGCTCA	180
TCCATCCAAT CAGCCACCTT TCTCCCTTCA AAGAAGTGTC TTCATTTTTT TCCTTCTTTT	240
GTTATTTTTA TTGACTGCCC ATCACTGTTA TTAAATCCTT CCCTCTTTTT TTGAATGAAG	300
CAGCAGAGCC TTTTATTTTG TTTTCCTTGT TTTGTTTTTT GTTTTTGTGT TTCAGAAATG	360
ACAGGGCTGT ATCACAGCAG TCTCGAG	387

## (2) INFORMATION FOR SEQ ID NO:303:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

GAATTCGGCC TTCATGGCCT AAAAATTAAG CAAGCAATAC CTAGCCAATA GTTCTGCTTA	60
ACTTTTNGGT TAAGTATTTT GTTGGGATTC CTATAAATAA TTTTTCACAC AAAGTTTAA	120
ATTTCTGGTG TACTTTGACT CTCAACTGAG AGTGGATAGA GTTTTTCTTT TGAGGATTAC	180

ATCTTAAAAAT GTCCATCGCC TGGCTGGTTA TAAGCATTTG TCACCTTTTG AAGGTAAAAAT	240
ATACTCTGGC CCTTCTTGAC TCAGTTACAG GTCATTTTAG GTCCAGTAAT AAGAGTCAGG	300
TGTTTGGTTA TTGCTTTCAG AGTCAGACAA ATCTCGAG	338

## (2) INFORMATION FOR SEQ ID NO:304:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 478 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

GAATTCGGCC TTCATGGCCT ACGAAGAAAA AATATTTTNG AGAGAATTTC CCAGATTGAA	60
AGAAGATCTG AAAGGGAACA TTGACAAGCT CCGTGCCCTC GCAGACGATA TTGACAAAAC	120
CCACAAGAAA TTCACCAAGG CTAACATGGT GGCCACCTCT ACTGCTGTCA TCTCTGGAGT	180
GATGAGCCTC CTGGGTTTAG CCCTTGCCCC AGCAACAGGA GGAGGAAGCC TGCTGCTCTC	240
CACCGCTGGT CAAGGTTTGG CAACAGCAGC TGGGGTCACC AGCATCGTGA GTGGTACGTT	300
GGAACGCTCC AAAAATAAAG AAGCCCCAAGC ACGGGCGGAA GACATACTGC CCACNTACGA	360
CCAAGAGGAC AGGGAGGATG AGGAAGAGAA GGCAGACTAT GTCACAGCTG CTGGAAGAT	420
TATCTATAAT CTTAGAAACA CTTGAAGTA TGCCAAGAAA AACGTCCGTG CTCTCGAG	478

## (2) INFORMATION FOR SEQ ID NO:305:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 568 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

GAATTCGGCC TTCATGGCCT AGACGAGCGG AGTAAATCT CCACAAGCTG GGAACAAACC	60
TAGTCCCAAC TCCCACCCAC CGGCGTTTCT CCAGCTCGAT CTGGAGGCTG CTTGCCCAGT	120
GTGGGACGCA GCTGACGCCC GCTTATTAGC TCTCGCTGCG TCGCCCCGGC TCAGAAGCTC	180
CGTGGCGGCG GCGACCGTGA CGAGAAGCCC ACGGCCAGCT CAGTTCTCTT CACTTTTGGG	240
AGAGAGAGAA AGTCAGATGC CCCTTTTAAA CTCCTCTTC AAAACTCATC TCCTGGGTGA	300
CTGAGTTAAT AGAGTGGATA CAACCTTGCT GAAGNTGAAG AATATACAAT ATTGAGGNTA	360
TTTTTTTCTT TTTTTTTTCA AGTCTTGATT TGTGGCTTAC CTCAAGTTAC CATTTTTCAG	420
TCAAGTCTGT TTGTTTGCTT CTTCAGAAAT GTTTTTTACA ATCTCAAGAA AAAATATNTC	480
CCAGAAATTG AGTTTACTGT TGCTTGATT TGGACTCATT TGGGGATTGA TGTTACTGCA	540
CTATACTTTT CAACAACCAA GACTCGAG	568

## (2) INFORMATION FOR SEQ ID NO:306:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 349 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

GAATTCGGCC TTCATGGCCT AATCAAAAAT ACCTTACCTT GTTCTGCCCT GTGAAAGTAG	60
CCTAAGGCCT GTCAAAAACA CAAAGAGCCC AAACATAATA AAAAAGATTA AAGAAGACAA	120
TATTAAANAA GCATTGTCTC AAAGATCTAC TGCTATATTA TATTTAAGTC AGGAAGTAAA	180
TCATCTTAAA ATAATGGTCA CTTCTTCAAC AGTGAGAGTT AACACCCAAA GTGAACGTAA	240
CACTTCAATC ATCAAGATTA CAATATATGG ACTACTTCTG GTAATAACTT GGTGCTGTT	300
TAGAACTTGT ACCAAACTAA CATCATGTGC AGAGAGGAAA GAACTCGAG	349

## (2) INFORMATION FOR SEQ ID NO:307:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

GAATTCGGCC TTCATGGCCT AGTGATGGGG ATGTGATGTG GGCATCTGCT AATTCGTCTG	60
CAACTACATG ACCTAAGATG GCCTCATTAA TCTAAGGGGC CTCAGCTGGA ACACTTGCCT	120
CTGCTGGATA ACCCAGGTCT AGTGTTATCC TCCAGACTAG ACCTGGCTTC TTCTGTGGCA	180
GTCTCAGGGC AGTGTTCCTA GACGGTGAGA GCAGAAGCCT AGGTTTGGCC ACATATCCCT	240
AACTCATAGG ATGGTGACAT AAACCTCTACC TCTTATGGAG AAATAGCAAG TTACTGCA	300
TACGGGACGA CTCGAG	316

## (2) INFORMATION FOR SEQ ID NO:308:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

GAATTCGGCC TTCATGGCCT AGTGGCAACG ACTTGGACAT CTGAGCTGTC ACTGCCGAAA	60
ACAGGCCGCA AGAGAGATAA TCAATATGCA TTCCAAGCC TTTTGGCTAT GTTTGGGTCT	120
TCTGTTTCATC TCAATTAATC CAGAATTTAT GCATGATGAT GTTGAGACGG AAGACTTTGA	180
AGAAAATTCA GAAGAAATTG ATGTTAATGA AAGTGAACCT TCCTCAGAGA TTAATATAA	240
GACACCTCAA CCTATAGGAG AAGTATATTT TGCAGAAACT TTTGATAGTG GAAGGTGGC	300
TGGATGGGTC TTATCAAAAG CAAAGAAAGA TGACATGGAT GAGGAAATTT CAATATACGA	360
TGGAAGATGG GAAATTGAAG AGTTGAAAGA AAACCAGGTA CCTGGTGACA GAGGACTGGT	420
ATTAAATCT AGAACAAAAC TCGAG	445

## (2) INFORMATION FOR SEQ ID NO:309:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

GAATTCGGCC	TTCATGGCCT	AGAAGTTCCT	TATGCTACTT	TCACTGAGCA	TCCTATGAAA	60
TACACCACTG	AGAAATTCCT	TGAAATTTGC	AAGTTGTCTG	GGTTCATGTC	TAAGCTTGTT	120
CCAGCTATCC	AGAATGCCCA	CAAGAATTCA	ACTGGATCTG	GAAGAGGAAA	GAAACTGATG	180
GTGTTAACTG	AACCCATTTT	GATTGAGACC	TACACAGGGC	TGATGTCATT	CATTGGAAAC	240
CGCAACAAAC	TTGGCTATTC	CCTTGCCCGT	GGGAGTATTG	GTTTTTGAGA	GTCTTTTGG	300
TACCATAAGC	ATATCATCCA	CAGATATGTC	ACTTTGAAAA	TTCCAGTTTG	ACCCACGCTA	360
TTTTTGACT	NAAACAATTA	ATTATTTTAA	AATGACGCTT	TATGATTTAG	AAATTAGTA	420
TTCCGAAAA	TTTAAAAGCT	TGATTGGACT	GATAGATACA	CACTTTAGAC	CTCATACAAG	480
AATAATCAAA	TTTCTTAAA	ACTAGAAAAT	AAATGCTGCT	GATACCTCGA	G	531

## (2) INFORMATION FOR SEQ ID NO:310:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

GAATTCGGCC	TTCATGGCCT	ACACTCATGC	TGCCAGTCCC	CAAAAGACTT	CATTCATTCA	60
ACATATATGT	GACCGCCTGC	TACGTGCCAG	GCGTGGGCCA	GGTCCTAGGG	ACAAAGGAGA	120
GGCCTCCGCA	CCCCACCCCA	TGACCCATAC	CTCCTCTTCC	CCACCTCCCT	GGGCCAGCCT	180
GCCTTCCTTC	TCCCTCCTCC	TCCTTCCTGG	GGGAAGGAAG	CCCCACCTTC	TGTGCGCAGT	240
CAGCTCCTAA	GCACGCTCCC	GCTTCCCTCG	GCCTCCCAT	TTAAAAAGGG	AGGCAAAGGA	300
TGTCACCACT	GTCACCTAC	TCATGGCTTT	GCTCTGGGAA	GTCCTGCAAA	TAAATGAAA	360
GTCTCTCAAC	CCGTACTCGA	G				381

## (2) INFORMATION FOR SEQ ID NO:311:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

GAATTCGGCT	TCATGGCCTA	CTTTGACGCA	CCAGGCACAA	CCCAGAAAGA	CGAGATTGTG	60
GAAATCCATG	AGGAGAATGA	GGTCGCATCT	GGTACCCAGT	CAGGGGGCAC	AGAAGCAGAC	120
GCAGTTCCTG	CACAGAAAGA	GAGGCCTCCA	GCACCTTCCA	GTTTTGTGTT	CCAGGAAGAA	180
ACTAAAGAAC	AATCAAAGAT	GGAAGACACT	CTAGAGCATA	CAGATTAAAG	GGTGTCAGTG	240
GAAACTGTAT	CCATTCTGTC	AAAGACTGAG	GGGACTCAAG	AGGCTGACCA	GTATGCTGAT	300
GAGAAAACCA	AAGACGTACC	ATTTTTCGAG	GGGCTCGAG			339

## (2) INFORMATION FOR SEQ ID NO:312:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

GCCTGCCTCG AGTCTTGGAT ACATCACACT TGAGTCAAAT CCTGGATACT GCCAAAGGAA	60
CCTGAAAATC CAGGAGACAA CGCTAGCTAT TCCTGTGAAC CTCTAGAGGA TTTGCGCCTG	120
CTCTTCAAAC AACAACCAGG AGGAAAGTAA CTAAAATCAT AAATCCCCAT GGCCCTCCCT	180
TATCATATTT TTCTCTTTAC TGTCTTTTA CCCTCTTTCA CTCTCACTGC ACCCCCTCCA	240
TGCCGCTGTA TGACCAGTAG CTCCCCTTAC CAAGAGTTTC TATGGAGAAT GCAGCGTCCC	300
GGAAATATTG ATGCCCCATC GTATAGGAGT CTTTCTAAGG GAACCCCCAC CTTCACTGCC	360
CACACCCATA TGCCCACT CGAG	384

## (2) INFORMATION FOR SEQ ID NO:313:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 547 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

GAATTCGGCC TTCATGGCCT AGGGGGGTGG GCTGATGGAG GGTAAGTAAA ACCTCCTACT	60
GGAAGATGTT CTCCTAAGAG TTCCACTTCA TTTTCTATCC TTTGCAGAGG CGATCGTGAT	120
TGCTGTGTTT GGAAGGGGAC AACTGGCCT GGTGGTGGCA AATGAGGAGG ATGATGGGGA	180
GAAAGGTGAG GAGGATGTAT AAGAAATGGA TCACTAGAAA TAAGGGGTGG GAATGCAGCA	240
TATGGTACTG GTAAGTGCTG AACTGAACAT GCCTGAAGCA TTGGAGGAGG CACACTACAG	300
ACAGGGAGGT GCTGTCCACT GAAAACCACA GAGCATCCTG GGACCTGCTG TGTACTACAA	360
GCAGGGATGT GCTGGCCTGT GCAGAGTGGG ATCCCATGTG GTGCCACTGT TGTACTGTG	420
TAAGAAACAG GGACTGTTCC TTGATGGAGC TGATCATGTA TGTCACCAT GACTGCATTG	480
TGCTGGGGTG GATGAGCAGC AGGATGTAGC AGACGGGGAG ATACATTCGG AGGGTGAAG	540
GCTCGAG	547

## (2) INFORMATION FOR SEQ ID NO:314:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

GAATTCGGCC TTCATGGCCT AATTTGTGGC TTACCTCAAG TTACCATTTT TCAGTCAAGT	60
CTGTTTGTTC GCTTCTTCAG AAATGTTTTT TACAATCTCA AGAAAAATA TGTCCCAGAA	120
ATTGAGTTTA CTGTTGCTTG TATTTGGACT CATTGGGGA TTGATGTTAC TGCACTATAC	180
TTTTCAACAA CCAAGACATC AAAGCAGTGT CAAGTTACGT GTGCAAATAC TAGACTTAAG	240
CAAAAGATAT GTTAAAGCTC TAGCAGAGGA AAATAAGAAC ACAGTGGATG TCGAGAACGG	300
TGCTTCTATG GCAGGATATG CGGATCTGAA AAGAACAATT GCTGTCCTTC TGGATGACAT	360
TTTGCAACGA TTGGTGAAGC TGGAGAACAA AGTTGACTAT ATTGTTGTGA ATGGCTCAGC	420
AGCCAACACC ACCAATGGTA CTAGTGGGAA TTTGGTGCCA GTAACCACAA ATAAAAGAAC	480
CACACTCGAG	490

## (2) INFORMATION FOR SEQ ID NO:315:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

GAATTCGGCC	AAAGAGGCCT	AGGAAGTAAC	AGTGTATCAT	GTATGCCACT	GATTCCAGGG	60
GACACTCCCC	TGCTTTCCTC	CAACCTCAGA	ATGGAAATAG	TCGTCACCCA	TCTGGCTATG	120
TTCCAGGGAA	GGTTGTCCCA	TTGCGTCCCC	CTCCTCCTCC	AAAGAGTCAA	GCTTCAGCCA	180
AATTTACCTC	CATCAGACGA	GAAGACCGGG	CAACCTTCGC	ATTCTCACCT	GAAGAACAGC	240
AAGCCCAGAG	AGAAAGTCAA	AAGCAAAAGA	GACACAAAAA	TACTTTTCATT	TGTTTTGCTA	300
TTACTAGTTT	CTCATTTTTT	ATAGCACTTG	CAATCATTTT	AGGAATATCC	TCAAAATATG	360
CTCCACTCGA	G					371

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

GAATTCGGCC	TTCATGGCCT	AATTTAAATG	TGGACAGATT	GGAGGGGAAA	GCTTTGCAGC	60
AAAAATCATA	AGTAGAAGGA	AACAGAAATG	TTAAGTACAC	AGTGTAAGTAG	CCATTTAGGA	120
AAGTTATAAG	CCATTTAAAT	GCCATGTATA	AAGTGTTTTT	GATAAGAAAA	AATCAAAGTG	180
TAAAGGAGAA	TACAAAATTA	TATGTGTACT	GCGGACACAT	CTGTATTGTT	CTGTGTATGG	240
AAAACAGACT	GGGGAGAAAT	AGCTTTAAGT	CCTAATAGTA	ATTTTCTTTT	TCTCTCTTCT	300
TTTTTCTGCT	TTCTCTTTTC	CCTGTCTCCC	TCAATATTGC	ATATCTTTCC	CATTAAAAAG	360
TATTGTATTA	TATATCTACC	AACAAGACAT	TTGTTTCAGA	TTTTTTGGTT	TTGTCTTCAA	420
GGAACATTCT	TCTGCATACA	AACTCGAG				448

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

GAATTCGGCC	TTCATGGCCT	AGAGATGGGG	TTTTGCCACG	TTGCCCAGGC	TCATCTCCTC	60
GAACTCTTGG	ACTTAAATGA	TCCTCCCGTC	TTGGCCTCCG	AAAGTGCTGG	GATTACAGGC	120
ATGAGCCACA	GTGCCCAGCC	TCTACCCGCT	TTCTGTGGTC	AGAAATAGAC	GCAGGACATT	180
CCATCCATAC	CTTATTCTTT	TCCTGGCTCT	TCTCCCATGT	GTCCTCGTGG	GTCCTGGTCA	240
CCCTCTTAGC	TGCTGTGTAA	TAACCCCTGT	GCAGATGCAG	CAGCCACGAT	GTCATCAGTC	300
CCCACCCAGT	GATGCATAGG	GGGCTTCTTC	CCCTCCCTGG	GTACAGCACT	ACCAATTCCT	360
GTGTATGGGC	CGTGTCAAGC	AGGGGCCACG	TCCTGGCCCC	GCTTCAGTCC	CGGCTCGGGC	420
TCCTCGCCGG	GGTCTCCATG	CCACTTCCCT	CTCCCATCTC	CACATCTCGA	G	471

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

```
GAATTCGCCT TCATGGCCTA CAGCATCGTC GGGACCAGAC TCGTCTCAGG CCAGTTGCAG      60
CCTTCTCAGC CAAACGCCGA CCAAGGAAAA CTCACTACCA TGAGAATTGC AGTGATTGTC      120
TTTGGCCTCC TAGGCATCAC CTGTGCCATA CCAGTTAAAC AGCTGATTCT GGAAGTTCTG      180
AGGAAAAGCA GCTTTACAAC AAATACCCAG ATGCTGTGGC CACATGGCTA AACCCTGACC      240
CATCTCAGAA GCAGAATCTC CTAGCCCCNC AGAATGCTGT GTCCTCTGAA GAAACCAATG      300
ACTTTAAACA AGAGACCCTT CCAAGTAAGT CCAACGAAAG CCATGACCAC ATGGATGATA      360
TGGATGATGA AGATGATGAC GACCATGTGG ACAGCCAGGA CTCCATTGAC TCGAACGACT      420
CTGATGATGT AGATGACACT GATGATTCTC ACCAGTCTGA AGAGTCTCAC CATTCTGATG      480
AATCTGATGA ACTGGTCTCG CTCGAG                                         506
```

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

```
GAATTCGGCC TTCATAATTT TTCTTATCTT CATTCTTTTC GGTGCCCAA TAAGCTCATG      60
TTTTCCATGG TCGGTTTAGT TTTTACTAGT CGTTGGCTAG TTTCTAATT GCATGTGAGT      120
TAGCATGTGG TGATGGCGGA GTAATGTCAT GTCTGGAGA GAACATTGCT TGAGTTCCAA      180
ACTTAGCTTT TCTACTTCTT GGTGAGACTT TGGACAAATT ATTTTGTAGC TTGTTTCCTC      240
ACTTAAAAAA ATGGGGTTTG TACCTTTAGT TGTTTCAACT GTTGTGAGGA CTTGAATAAT      300
AAAGTATATA GCTATAGATA AGAAAACCTG GGGGACTCGA G                                         341
```

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

```
GAATTCGGCC TTCATGGCCT AATTTTTTTC AAAACCTTGA AATGACATGT TAAATGCTG      60
CTTTGAACCTG GTTTTCTTT AGCCTGTAGA AAAGAACTTT GAGTTACTGG TCAAGTAGTT      120
TTGACCATAC TGGCTTAGGA AAACAGCGCA TCAGCTGTCT GATTGCTATC ATGTAAAAAT      180
CTGTGAACGA CTTTGAGAAG TCATTGGTGG ATTATGTTGT TCAGGAATAG GAATGGAGCT      240
TTCTTCCTAT CACTGTGATT TTTTTTTTTT TTTGGAAGGG GGGAGGAGGA GGAATTATTT      300
CCNCCCTAAT AAANGGNGGN NTTAATCCTG GGCCCCNNNA AGGCTGGNNN GGGTCCNGAT      360
KTGGGGGTNC NNTTTATTGG GAACTGACNG GGNTTTAATT TTCCGGTTTT TTTTTTTTCT      420
TGAATGATCT TGTGTGTAG AGTTGAATAC AGTTCTAGGG AAGTATGATC ACAAATGAA      480
TGTGGCAGT TCCTCCTATG ATTAATATGT CAGACATGTC AAAATTCTCT CATCATGTGT      540
```



ATTGCGGGG TTTATTTCAGT CCAGGACTCG AG

572

## (2) INFORMATION FOR SEQ ID NO:321:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

GAATTCGGCC	TTCATGGCCT	AGATAACTTT	GAACAGAATG	GGAGGCAGGT	TTACCCTAAG	60
CAGTTCCTCA	CTTGAAGTTT	TCCTTTAGTT	TAGTGATTTG	AGGGGCCCAA	AATACTTTCA	120
CATTTCCCCC	CTTTCTTTT	TAAAAATCTG	TTGGAGAACG	CATTTTAGAA	GAAAATGAGT	180
CTCTGGCCTC	AGGTTTCGTC	TGATCTCTCA	TGGCTAGGAT	GGTTTATTCC	TAGATAGATA	240
GGTCCTGAGT	TATTAGGAAA	GCTCCTTTTT	AGAAGGTGT	GAAGTCTCAT	GTCCTGTGAA	300
GAGAAAATAG	GGGGAGGACA	ACAACAAACA	AAAGAACTCG	AG		342

## (2) INFORMATION FOR SEQ ID NO:322:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

GAATTCGGCC	TTCATGCCTA	CAATATGTGT	TAATAATTAT	TCAGAAATAT	TCAAGTATAA	60
TACTTAATAA	AAATTCTGTC	TATGTGCAAG	GCATGGTGCT	AGGTACTGAG	ACTATAAGGA	120
GGTAAAAGAT	AGTTCCTGCC	CTTAAAGACT	TCTATAATTT	AATCAGAAAG	GAGAGTATAT	180
GAAAATCATA	CTGAATAAAA	AGTGGCTCAT	AATAAATGCC	AAGGAATCAA	CACAAAGTCC	240
TTTCCCTGGT	AGGGAAAAGT	TTTTTGAGGA	AATGGGACAT	GAATTGGCT	TTGAAGGATG	300
TGGAGGTTT	AGATAAGAGG	GAGAACTGT	TGTGTTCTAG	GTTAGAGGAA	CAACATAAAC	360
TCAAAGAGA	CTAAGAAGA	ACGGACTCGA	G			391

## (2) INFORMATION FOR SEQ ID NO:323:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

GAATTCGGCC	TTCATGGCCT	ACCCTGAGCA	GTGCCTGGCC	CATACTGGAT	ACACAGTGTG	60
CATTTTGTGG	GGACTCAAGG	AAGGAAGGTA	ATATCCAGC	TCAGGGTTCT	CTCTGACCCT	120
GAATAGTGTT	ATGGACTCTT	TGGGAAGGAT	AGAAGCTTTC	TTAGTTTTCT	GACAGAGGCC	180
TGTAGGCTGC	AAACGTTGTG	TTTGTAGAAA	GAGTTGTAAA	GGTGTCATGA	GCCTTTATTT	240
AAAAGTGTCT	TTAATGTATC	TTAGGCATCT	TTTTCTTTC	ATCTCACACT	ATGGACAGTT	300
TTAAGTGCAA	AAGGGGA	ACTCGAG				324

## (2) INFORMATION FOR SEQ ID NO:324:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

```

GAATTCGAGC TCGACTGGAT AGTTTTTCTT TTAAACTTA AAATGCTTTT TAGTTTGGCA    60
CTCCGTAGTA AAGGAGGTTC CAGAAGCCAG TAAGAGAACC TCTGCCAACT ATGAAAGAGA    120
AGATATTTCT ATCTACAAGT TATTTTCAGGA TCAATTATTC AATTAATATT TTATATAATA    180
GAAAGGTTTT ATTTGTTAGG ACTTTATCTT TAAGTTCCTC AAGAGTAAAA AGGTCTAGTC    240
ATTATTATAC TGTGGGAGAA TGATAGAAGA TTGATTACAT TGAAGTCCA GAACCTCTAT    300
TTATTAAAAA GATTTAAGAT TTGACACACT CTCGAG                                336

```

## (2) INFORMATION FOR SEQ ID NO:325:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

```

GAATTCGGCC GGCATGGCCT AANCTAAAAA TAAATNAAC CCAACGCATA NAANACGGGT    60
TTATCTCTCC TAAAAACANT TNAGTTTNGA CTAAATGAA ACANATCATN NNACAACNTC    120
ATTTTNAAT GAAGATTTTA CCTGGACCCT AGGTGTGCTA TTCTTCCTAC TAGTGGACAC    180
TGGACATTGC AGAGGTGGAC AATTCAAAAT GAAAAAATA AACCAGAGNA GATACCNCG    240
TGCCACAGAT GGTAAAGAGG AAGCAAAGAA ATGTGCATAC ACATTCCTGG TACCTGAACA    300
AAGNATAACA GGGCCAATCT GTGTCAACAC CAAGGGGCTA GATGCAAGTA CCATTAAAGA    360
CATGATCACC AGGATGGACC TTGAAAACCN GNAGGAAGTG CATCTCGAG                                409

```

## (2) INFORMATION FOR SEQ ID NO:326:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

```

GAATTCGGCC TTCATGGCCT AGGCGGCGGC AGCCGAGGGC GTACTGGCGA CCCGGAGTGA    60
TGAGCCCGCC CGAGACGATG CCGCCGTGGA GACAGCTGAG GAAGCAAAGG AGCCTGTGTA    120
AGCTGACTTC ACTGAGCTCT GCCGGGACAT GTTCTCCAAA ATGGCCACTT ACCTGACTGG    180
GGAAGTGACG GCCACCAAGT AAGACTATAA GCTCCTGGAA AATATGAATA AACTCACCAG    240
CTTGAAGTAT CTTGAAATGA AAGATATTGC TATAAACATT AGTAGGAAC TAAAGGACTT    300
AAACCAGAAA TATGCTGGAC TGCAAGCTTA TTTGGATCAG ATCAATGTCA TTGAAGAGCA    360
GGTAGCAGTT TTTGAGCAGG CAGCTTACAA GTTGGATGCA TATTCAAAAA AACTGGAANC    420
CAAGTACAAG AAGCTGGAGA AGCGATGAGA AACTTATTTC TATGGGACAG AGTCTTTTTT    480

```

TTTTAATGTG GAAGGACTCG AG

502

## (2) INFORMATION FOR SEQ ID NO:327:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 468 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

GAATTCGGCC TTCATGGCCT AGAATATTCC ATATCAGTAC ATATAGCACT GCCTCACTTT	60
TTAATGGCTA TATAAATAG TACTATAATT TTAAACCACT CACCTGATGG TGGGCTTAGT	120
AGTTATTCTG TGGCTGTAAC CAACATCACT GCCATGTGCA CTGGTACACA TACAGAAGTC	180
CACACAAGTA GGCCTGTATC TGTAAAGTAA ATACTGGTGG GATTACTGAG TGAAAGGAGA	240
CGTGAATTTT TAGATTTTTA CTATGAAAGA CAACTGCTC TTTATGGGGA TTTTATTAAT	300
CTACAACCCC ATCAACAATG TATGAGAGCC CATTTTTCAC ACACTTGCCA ACTCAGTAGG	360
TTATTAAACC TTTTGGTCTC TGCCACTTGT ATATCCCAGA TCAACTTCTA ATTCTGCTTC	420
ATATTGTTG CTATCCTTA GAATATTCT GTCCACCTT GTCTCGAG	468

## (2) INFORMATION FOR SEQ ID NO:328:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 300 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

GAATTCGGCC TTCATGGCCT AGGGAAAGGA AGTGACATAG TGGTATAAAA ATTTGAAATT	60
TGTGATGTGG CTTAGAAGCT TGATATATAC GGGTATGATT GCAGCTGCTA CATTTAGCCT	120
TTTTTCTTT CTTTTGGAG AATGAACCGC ATTAAGAAAT ACATTTTACA TCACAATTTA	180
GCAAGTATAT GTGCTAACAT ACTTCTGTTT CTACAAGGGA TGTATTGTGG TATTTCTAT	240
TGCATTTTAC TCTAATTTAG TTCATTAA AAAATGCTGA TTCTAACCCA TGAAGTCGAG	300

## (2) INFORMATION FOR SEQ ID NO:329:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 306 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

GAATTCGGCC TTCATGGCCT ACCACCACAC CCGGCTAATT TTTTGTATTT TTAGTAGAGA	60
CGGGATTTC AATGTTAGC CAGGATGGTC TTGATCTCCT GACCTCGTGA TCCACCCGCC	120
TCGGCCCCC AAAGTGCTGG GATTACAGGC ATGAGCCACC GTGCCTAGCC GACTCTTGAG	180
TTTTGACAAG AGGTGATATC TGGGAGATTA ATAAGTATTT AGTTTAAGAA AACATTTAGT	240
AAGCCTGTCC TGTGTTCCCA CACAAAGGGT ATAACAGCAA TATATTCCAT AAGAGTAAAG	300
CTCGAG	306

## (2) INFORMATION FOR SEQ ID NO:330:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

```

GAATTCGGCC TTCATGGCCT ACATTACCAT CAGATTGACA TATTTAATTA TCAGATATCT      60
TTCTTTTGCC AAAAAGTTGT GGTGAGTTG GCCCTGGGAT TTATAAATAC ATGCACACAG      120
CACATTTCTG TCATTGTTCA CTGCAGTCTT TTAACACATC TTCTCAGCAA TATTCTTAAT      180
GTTTCACGCG GGAAAATTGT AAATTATTTA ACCACTGAAT TAGAGGTGTG TTGTTTTTTA      240
GCTAATCAAT AGCCATTGAA TGCTTAAATG GGCTTTAAAG TAGACAAAAG TAAAAGACAG      300
CAAAGAAAAT TAATCAGTAA GATTGCCCAT ACTCCATAGA CACTTGAGCA GCTACTTTAG      360
TCATTTTGAA ATACACGCTT TATGTTTTC CTTGGACTGG CATATTCCTG TCATTTATAA      420
AAAGAATATA CATTGTGAAA TTTAAGGTGT GGACATTCAT TATTGAAGGT AGAAATAGTT      480
ATAATCATCA GTGTCTAGAT ATATCTGAAG AGAGGTACTC GAG                          523

```

## (2) INFORMATION FOR SEQ ID NO:331:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

```

GAATTCGGCC TTCATGGCCT AAAGTAGGCA AGGGATAATA ACCAAAGAAG NAAATTTTCAT      60
GAAGACTAGA CATCATAAAG CATAATTTTA ATAGTCACTC AACCAAGTAT TTTTATTTT      120
TTATGGATAC TCTGAATGGC AATTAAATGT GAAACCCAGT TTCTTGGGCA AGTCAAATTC      180
TGGAATCACA TCCACCTAAA TTAAATGAC TAGCTCGTAT TTTCCCATC TTCAAGTTTC      240
ACATCCTGGT CATCAAAGA CTCGACAGCA AGACTTAGAA TGAAAAAGGG TACTTGTTTA      300
TATTAATATT TTTTACTTGA ACACGTGTAG CTTGCAGCAG GTTCTTGATG AATGTGCTTT      360
GTGTCCAAAA TGCCTCCCA TTGTACACAG GTGTACACCA TGCATGCACC AACACCCTC      420
GAG                          423

```

## (2) INFORMATION FOR SEQ ID NO:332:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

```

GAATTCGGCC TTCATGGCCT ACAAGCCACA AAAGTGTGGT GAATGGAAAA GAATGTATAA      60
ACTTCGCCTC ATTTAATTTT CTTGGATTGT TGGATAACCC TAGGGTTAAG GCAGCAGCTT      120
TAGCATCTCT AAAGAAGTAT GCGTGGGGA CTTGTGGACC CAGAGGATT TATGGCACAT      180
TTGATGTTCA TTTGGATTGT GAAGACCGCC TGGCAAAATT TATGAAGACA GAAGAAGCCA      240

```

TTATATACTC ATATGGATTT GCCACCATAG CCAGTGCTAT TCCTGCTTAC TCTAAAAGAG	300
GGGACATTGT TTTTGTAGAT AGAGCTGCCT GCTTTGCTAT TCAGAAAGGA TTACAGGCAT	360
CCCGTAGTGA CATTAACTTA TTTAAGCATA ATGACATGGC TGACCTCGAG	410

## (2) INFORMATION FOR SEQ ID NO:333:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

GAATTCGGCC TTCATGGNCT ACCTTAGCCT CAGCTCTTTC TTCTGGGTTG TTGTATTTT	60
CTTTTCTGTC CCAAACAGTT TCCCCACAA AAAGAACTTT ATGTCTTCT CTGTCTTCCC	120
TCAGTCCTTC CAGTCAGCAG CCTGTGATTG GGCTTTTCCC CTCAGAAACG AACAATCCAG	180
AACCCACTGT TTAACAAC TGTATTTTGC CTGGGAAGT CCCATTGCCT TCCCTGAAAA	240
CATTAAACAT TCCTCCGATC CCCAGCCTGA GTCTCTCTGT CTCTGGGCCC CATCCTGCTC	300
CACAGCAGGG CTGGTGTGTC CAGCACAGAG TGACCTCCG ATGCCCTTTC CCACCCGCCG	360
CCNTGCCTCC CTCGAG	376

## (2) INFORMATION FOR SEQ ID NO:334:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

GAATTCGGCC TTCATGGCCT ACGGGTTGTT ACATATTAT TCTTTTTTGA AGCCCATCAC	60
TACATCGCCA TTACGTTTTA CACTGTGTAT GTAACAAATG TTACCACTTT GTTCTTTATT	120
CCTTTTTTGA TCATCTTCAG TGGGGGTAAA ACAGTATCAA GCTCTAGAGC TCCCTCTGGT	180
GGTTTTTGTG ACATATTTGA AGATGGCAGC TTGCTTTTGT AGAATTTCTG GCTCTGCTCT	240
CCCTGTTTTT ATCTGTACTT TTTTCTCTCA TTGTGCCTCT TGCACACACA CACCCCCCCC	300
ACTCGAG	307

## (2) INFORMATION FOR SEQ ID NO:335:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

GAATTCGGCC TTCATGGCCT ACATTACTCA GCTTTCCTGA ACAACCAGGC ACGACCCTCT	60
GCCTGCAGGC CAGGCACGTG CTGCTGCCCC TGGAGGCGGG TGGGGGTGCC TCCGCGCTGG	120
AGGACACGGG GTGCACTGAG GCTTCCCAT TGGTATGGGG GAATGTGGTG ATGAGGGGAT	180
GCGGTGCCCG CGGACCGCAC ACATGCCATG TGTGGACACT CAACAGGAAG CTTCGGTCAG	240

CATTTCAGCT GGAAATGCAG AGCCAGGGCC CTGGAAAGTC CCTCAGCAGC TGTGCACAGG	300
CCTGCTCACC GTGCGTGTGC GGGCAGAGCC TCCCTGGGGA GGCAGAGGCC CCGCGTTCTG	360
CACTCGAG	368

## (2) INFORMATION FOR SEQ ID NO:336:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 437 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

GAATTCGGCC TTCATGGCCT AATTGAATTC TAGACCTGCC TTCCTGCTCT TCTAGGTAGT	60
CACACTTCAC TAAAGTGTCA TCCACCACTG TGTGAATCC GAAGAATGAC AATTTTCTAC	120
CACTGGTGTA AAAAACAAAC ATTTGAAGAC CCTTGTGCAT TGTGTGTCAC AAAGCTAAAT	180
ACATGGAAAT CGTTAATATC GCTGATATTA AGTAATTTCC CCACTCTGAG TGAATACTTT	240
GATGATTGCC AACAGTGGCT AATAAAATGA CGGCTACCAC ACTCATGGGT CACTGGGGCT	300
GCGCAGGGCT CTTTGAGGTG GGTGGCTTCT TTTGGAAAGT ACTATGAACG TCTCGAAGCA	360
GTATTCTAGT GATAAGAATT CTTAACATAG CCAAGCGCCC CACGTTTGTT CCCCACGTTT	420
GTTCCCTTA TCTCGAG	437

## (2) INFORMATION FOR SEQ ID NO:337:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 430 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

GAATTCGGCC TTCATGGCCT ACCAAACCCA ATTTATTTAA AAANATACTT CTATATCATT	60
ATATGTATTA CCAATTGTTT TAGCCTTATA CAGGATGCGG TGTNCTGTGC TCCTTNGTGA	120
ATGTCNGTTG CTGGTAGCTG GTTATGCTCA TGATGATGAC TGGGTTGACC CCACAGACAT	180
GCTTAACTAT GATGCGGCTT CAGGAACAAT GAGAAAATCT CAGGCAAAAT ATGGTATTTT	240
AGGGGAAAAG GATGTCAGTC CTGACTTGTC ATGTGCTGAT GAAATATCAG AATGTTATCA	300
CAAACTTGAT TCTTTAACTT ATAAGATTGA TGAGTGTGAA AAGAAAAAGA GGAAGACTA	360
TGAAAGTCAA AGCAATCCTG TTTTtaggag ATACTTAAAT AAGATTTTAA TTGAAGCTGG	420
AAAGCTCGAG	430

## (2) INFORMATION FOR SEQ ID NO:338:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 316 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

GAATTCGGCC TTCATGGCCT AGAAATAGAT TTTTCCTCAG ACTCTCATCT CACATTCCCT	60
---	----

TTTAAGATTT CCTNGTCCTA TCCCCACCCC AGACGTTTCC ATTTTGCTTT TATTTTCTAT	120
AATAATTCCT GGGGGCCTCT ATTAAAGGCC TTTTCTTTG ACTACTTACA TCCATTATAC	180
CAGTATCTTT GTCAGTAAAA TTTTATATAT CTTTATTCT GTCATCAGGT TAAGAAACAA	240
TAATTGTATT TTAAAGGAA AATATTTTAC GATGCTACTA AGCAGTTACT TTGTCCACTT	300
ATGCAGGATA CTCGAG	316

## (2) INFORMATION FOR SEQ ID NO:339:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 306 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

GAATTCGGCC TTCATGGCCT AGCTGGCTGG CACCTGGAGA ATCCCTGAGC TGGAAAAGCA	60
GCTTGGTCTG CAGAACTGAG TCACAAGACT GAGGCACTGG GGAGCCTCAG CCCCATCTGG	120
TTGTTGNTCC CTCTGTGACC TTGAGCTTGT CTTCCACTTG GTGCCGTAGG CCTTCATTTG	180
TCCATTGAAG TTAGCACCTG TCCCTCCCGT CCTCCAGAGA GGTCAGGAGG ATAAGCATT	240
GAAGACTCAC TGTGGTTTAT TGAGTGCTTA CTGTGCAGGT ACTGCTGTAG TTTTGTGCAA	300
CTCGAG	306

## (2) INFORMATION FOR SEQ ID NO:340:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 580 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

CAAACCTTTG AGTNNNACAG TTAAGATATT ATGTGAAGCT CAGAATCATG TTTCAGACCA	60
TTGAAATTAC TGGTTAAAT ACAATAGCT GAAGACATGA TGTAAGAT TAAGTACTTG	120
GTTTTGTAAC ATATTTACCA ATTAAAGTCA CAAAATATT CTCATTATT ATTCATGCAG	180
GTAAGTGA AAAAGATAGT GCAGAAATCA ACTTTAAATA AAAAATTATT CCTCCCCTTC	240
CTCCCACTCC CCTATACTCT ACAAATGTT TTCCCTGGGA CTAGGCCTTG AAAAGGCCAC	300
TACATATTAG TGTGACATGC ATTACTGTCT GCAATTAAAA AAGCTAACCT TGTGGTGATT	360
GTAATTACAT TATAAAAATG TCCACATGCA TAAATCTAAA AAAGGTTGAA AACCTACAGT	420
AAATCTACAA TATAGTGTAT ACATTTGACC ACTGGTTTGT GTTATGTAGA AGTCATAGAT	480
TTGGTAAAGC ATTGTAACAA TTTAGGAAGG CATCTAAATC TTTAAGTTCT GGACAAATTT	540
TATGTTTTAA TCTACAAAAT TGCATGAAGG CTAAGTCGAG	580

## (2) INFORMATION FOR SEQ ID NO:341:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 433 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

GAATTCAGAN TTNTGCTATG GTAGCACCAG ATGTCCAAAT TGAAGATGGG AAAGGAACCC	60
TCCTAATATC TTCCGAAGAG GGAGAGACGG AAGCTACTAA NTCACAAGAA GTTNTTCAGA	120
ATTTGGAATT AGAANTGGCA NCCGGCTTCA AGCAGATGAC TTCNTCCAGG ACTATACTTT	180
ATTGATCAAC ATCCTTCATA GTGAAGACCT AGGAAAGGAC GTTGAATTTG AAGTTGTTGG	240
TGATGCCCCG GAAAAAGTGG GGCCCAACA AGCTGAAGAT GCTGCCAAAA GCATAACCAA	300
TGGCAGTGAT GATGGAGCTC AGCCCTCCAC CTCCACAGCT CAAGAGCAAG ATGACGTTCT	360
CATAGTTGAT TCGGATGAAG AAGATTCTTC AAATAATGCC GACGTCAGTG AAGAAGAGGG	420
AAGCCAGCTC GAG	433

## (2) INFORMATION FOR SEQ ID NO:342:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

GAATTCGGCC TTCATGGCCT AAAACTCTAA TAGTCTCTCT TCAGCGGAGC CACTGAAGGA	60
AGATAAGCCT GTCAGTGGTC CTAGGAACAA GACTGAAAT GGACTGACTC CAAAGAAAAA	120
AATTCAGGTG AATTCAAAAC CTTCATTCA GCCCAAGCCT TTATTGCTTC CAGCAGCACC	180
CAAGACTCAA ACAAACTCCA GTGTTCCAGC AAAAACCATC ATTATTTCAGA CAGTACCAAC	240
GCTTATGCCA TTGGCAAAGC AGCAACCAAT TATCAGTTTA CAACCTGCAC CCAAACTCGA	300
G	301

## (2) INFORMATION FOR SEQ ID NO:343:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

GATTCAGATG GAGATGCCAA GCAGGCCCTT AGGTGAAGGA GTCTGGAGTC TGAAAGCATT	60
TGGGATGGGG ATATAGACTT GAGAGCCATC AGCTTATAAA TAGGACTTGG TCAAGAATGG	120
GTGGCCTCCA TCCTAGATGG ATATAAATAA GAAATAAATA TCAATTTTTT TTCTTATAAC	180
ATTCCTAGGT TTTTATTTTT ATGACTTTAA GAAAAATATG AATGACAAAA ATAAACATA	240
AAATCAAATA TATCCGTATT GCCCTTTGGG GGACACCATC TCTTGCTCAC TTTACACAGT	300
AAGTGCCATT TCCTTCACCT CCATGGAAAA CATTTCGTAA ATTACTAAGT TGAATAACTT	360
AAAATATAGG ACGGGACATC TCGAG	385

## (2) INFORMATION FOR SEQ ID NO:344:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:



GCAGAAACCT TCAGGGAAAC CCCATGCTAG CGGCAACTGC ACCACACTTT GAGGAGAGCT	60
GGGGGCAGAG ATGTCGTCGA CTCAGGAAAA ATACAGGGAA TCAAAAAGCT CTAGACAGTG	120
ATGCTGAGAG TTCCAAAAGT CAAGCAGAAG AAAAAATCCT AGGTCAGACT TATGCAGTTC	180
CCTATGAAGA CGATCATTAT GCAAAAGACC CAGACATTGA AGCACCCAGC AACCAGAAGT	240
CAAGTGAAAC GAATGAAAAG CCAACGACAG CTCTTGCCAA CACCTGTGGA GAGCTCGAG	299

## (2) INFORMATION FOR SEQ ID NO:345:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

GCATTTGGTT CTTTTATAT CTTCCTATTC TCTCACTATA TTCCTGTTTT TCTTTTAATG	60
CTTGACATC ATTAACTCG CTGTTATCCT TGTCTGTGAG TCATCTGGTC ATTTCTGTGT	120
GTTTTATTA ACTGATTATT CTCCTTGTCC TGGCCACATT TCTGTGCTTT TNGGCGTTTC	180
AGTAACTTCT GATTGGATGT TGGGTATTAT AAAGATTATA TTATTGAGTG TCTGGATTTG	240
GGGTGGTAGT TACTGTGGA TCAGTATGAT CCCTTTGAGG CCTATTTTGA AGCTTCAGCT	300
CGAG	304

## (2) INFORMATION FOR SEQ ID NO:346:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

GAATTCGGCC TTCATGGCCT AGATTACAAC ACGTGTGCCA CCACACCTGG CTAATTTTTC	60
TATTTTGTAGT AGAGACGAGG TTTCACCATG TTGACCAGGT TGGTGGTCTT GAATTCCTGG	120
CCTCCAGCCT GGTGACAGAG CGAGACTCCA TTTCAAAAA AAAAAACAAA CTTCATGCTG	180
AGAAAGTCTGA AGAAAAAATA GATTTTAAAG AGGAAAATGT GTAAGAAAAA TACTTCAGCT	240
TCTGTTACAA AATCAAAATA GAAAAAACA CAAATTTGGT GTTTCCTCGA G	291

## (2) INFORMATION FOR SEQ ID NO:347:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

GTAACCTTAG CTGTACCTTG CAAACCAGAA CATATGGTCA CCCTACCCTC CGGTCACTTT	60
TTCTTCTTTG TTTCATTCT TTTAATTTT TTCCCTTTTA AACACACAGC ATTATCTTTC	120
CCTGAGCACC ATTGTCTTTG CAAATGCTCT TGCAATCGGG ATATTTTGA CCTGGCAACA	180
TGCATATTCA GTCTGAACAG TCTCTCTGAA CCTACCCCAA AACCTGGTTT TAGCTTCCAG	240

GCAGAAGACT CTGTTCCCTG GCTTGCAACC CCCAAACTCG AG

282

## (2) INFORMATION FOR SEQ ID NO:348:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

GAATTCGGCC TTCATGGCCT ATATCAATGC AATTTTAAAT TTTTGTTAAT ATCAACAGCA	60
AAAGCCTAGT GCATTGGGAG ATGTGCAACC TCCCTGAAAA TCTTTTCTGT TTCTGGAGTA	120
CTTCAGGGGT GGCCTCTGGC CCCAGAGCCT TTGCCACAGT GCTCCCACCA GCCCCACCT	180
CATCCGTCTG TTTGCAGAGC CTCATCTACA GGTCCCCACG CTGCCTTCTT TACTCACTCT	240
GCGCTTGGCC GTTTTGTTAT TTGGCTTAGT CTACATTGGG CGGAAGTCTG TGTGCACAGA	300
GTGGGTGTTT CTTCGAGCCC CTTCCTCTCA GAGGGCCACA CG	342

## (2) INFORMATION FOR SEQ ID NO:349:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

GAATTCGGCC TCATGGCCTA CAAAGAGCTG GGATTACTGG TGTGAGCCAC CGTGCCCGGG	60
CTGGACATCT GGTTTAACT AGATGGAAGG GAAGAACATT ATGAATCTTT AAAATACGGC	120
TGTTGCCATT TTTCTCTCTT CTTAACATGC AGCATAGGTG ACAAGCTTTT CTGTCATCAT	180
CATGGAGCAT TCTGAATCAT GACATTTTGT TTTGAGAGTT CATTCTTGAA TTTTCAGTTC	240
AAAATATTGT TTGAACTATT ATTCCACATT CAAAGATTAT ATAAGGTCCT GTGCTTTTGA	300
ATCTTTTTCA AAAAATTAT TTCTGCCTGC TTAACAAAAA TACTTTTATT TCCCCACAGA	360
GAGTTCAGGA CTTAGATTA GTTTGTGTTC AGCTCACTTA ACTGGATAGA CAATTTTGCG	420
TTTTGCAACA CCATAGCTCG AG	442

## (2) INFORMATION FOR SEQ ID NO:350:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

GAATTCGGCC AAAGAGGCCT AAAAAATGA AATTCCTTAT CTTGCATT TTCGGTGGTG	60
TTCACCTTTT ATCCCTGTGC TCTGGGAAAG CTATATGCAA GAATGGCATC TCTAAGAGGA	120
CTTTTGAAGA AATAAAGAA GAAATAGCCA GCTGTGGAGA TGTGCTAAA GCAATCATCA	180
ACCTAGCTGT TTATGGTAAA GCCCAGAACA GATCCTATGA GCGATTGGCA CTTCTGGTTG	240
ATACTGTTGG ACCCAGACTG AGTGGCTCCA AGAACCTAGA AAAAGCCATC CAAATTATGT	300

ACCAAAACCT CGAG

314

## (2) INFORMATION FOR SEQ ID NO:351:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

```

GAATTCGGCC AAAGAGGCCT AGCTACCAGA GTGTGAGAGA CCATTGTCTC GTTGGCTGGC      60
GCTCAGGAC ATGCAGTCAC GGTAGCGGA GCAATCACAA AACTGTAATT TACTTACCAA      120
ATCTCTTCTT TTCCGTAGCC TCGCCTGCCT GACTTAGAGA AAGAAAAGCA ATAATTTTAC      180
AGGCATTTTG AGGTGTCTCT TTGGGTTCTT TCTGTTTGAA AGGATATTTG TCGAAAAAAA      240
GAGCAAAACC GTTTTAAATA AACTCCCCCT GGAAAAAAC CCAAAACACT TGCATCTCGA      300
G                                          301

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## (2) INFORMATION FOR SEQ ID NO:352:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

```

GAATTCGGCC AAAGAGGCCT AGCAAATACA CATTAATAAG AATGCCTAGA AGAGGACTGA      60
TTCTTCACAC CCGGACCCAC TGGTTGCTGT TGGGCCTTGC TTTGCTCTGC AGTTTGGTAT      120
TATTTATGTA CCTCCTGGAA TGTGCCCCC AGACTGATGG AAATGCATCT CTCCTGGTG      180
TTGTGGGGA AAATTATGGT AAAGAGTATT ATCAAGCCCT CCTACAGGAA CAAGAAGAAC      240
ATTATCAGAC CAGGGCAACC AGTCTGAAAC GCCAAATTGC CCAACTAAAA CAAGAATTAC      300
AAGAAATGAG TGAGAAGATG CGGTCACTGC AAGAAAGAAG GAATGTAGGG GCTAATGGCA      360
TAGGCTATCA GAGCAACAAA GAGCAAGCAC CTAGTGATCT TTAGAGTTT CTCATTCCC      420
AAATTGACAA AGCTGAGCTC GAG                                          443

```

## (2) INFORMATION FOR SEQ ID NO:353:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

```

GAATTCGGCC AAAGAGGCCT ATAGGCNTCT TTGGCCGGCC AAAGAGGCCT AAAAAATCT      60
CAGCTATGGT TCATTATTAC TAGCTCAGCT TTTAATTCTT TAAATTGGTT GAATTATTCT      120
CTATGTCAGT TATTTTATT GACCAGTTT GGAATATTTT TGTTCAATTA TCAGGGAGTA      180
TGCGGTTAAT GAAGTTGTGG CAGGGATAAA AGAATACTTC AACGTAATGT TGGGTACCCA      240
GCTACTCTAT AAATTTGAGA GACCACAGTA TGCTGAAATT CTTGCAGATC ATCCCGATGC      300

```

ACCCATGTCC CAGGTGTATG GAGCGCCAAC TCGAG

335

## (2) INFORMATION FOR SEQ ID NO:354:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

GAATTCGGCC AAAGAGGCCT ACAGAGATTA TATTGGGGTT NCCATTTTGT GAAGCCANAG	60
ACATNTGGTC ATTGGGATGT GNGATTGCAG AATTATTTCT TGGANGCCCG NTNTACCCAG	120
GAGCCTNGGA GTATGCTCAG ATTCGANACA TTTCTCAGAN TCAAGNTTNN CCAGGAGNAC	180
AGTTGTTANA TNTGGGTACT AAATCCACAA GATTTTITG ACANAGAAAC AGATATGTCT	240
CNTTCTGGTT GGAGATTAAA GACACCGGAA GAGCATGNGG CAGAGACTGG AATGNAGTNT	300
TAAGAAGCCG GACTCGAG	318

## (2) INFORMATION FOR SEQ ID NO:355:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

GAATTCGGCC AAAGAGGCCT AGTGGGAATT TTAAATACAA GATCCTGTTG AAAATATTGA	60
TATTCAAAGA AACAAACAGC TTTGGATCCA TAGCCACAAT TTAGGTTTTT CTAGATTAAA	120
ATCAGAAGTG ATTTTATTGT TGAAGATAC ATTAATTCTT TGAAGTCAGA ATAAGAGGCT	180
TGACAATTTA ATTTCTAATT AAGTGACTGA ATAGACAAAG GATCAAATAC AAACAGTAGT	240
GCAGGAAGAA AATAAATTGG AAGAAATAAT TGTTCACCA GTAGTAATAA TTAAGACCAC	300
CATTTTAAAA TTTTCTATAC ACAAAGAATG AGAAAATATT GTTATTATTA TTATACTCT	360
TTCTTCTTCA GTATTAGTGG ACCCACATTA TCTCCTGTCA ATTCATTGTG TTTATNATGT	420
GAACCATCTC TCGAG	435

## (2) INFORMATION FOR SEQ ID NO:356:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

GAATTCGGCC AAAGAGGCCT ACAGGCTCAC ATTGACTACA CACGTTTATA CCAGGCGCCA	60
TGTTCTTTGC CGAAACTCCC GCTCAGAGCC TGGATGATCT GCCCCTCACC TCTGCCCTCG	120
TTCCCATCCA CTCTCCCCTC CTGCTCTGT TCCTCGAG	158

## (2) INFORMATION FOR SEQ ID NO:357:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 303 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

```
GAATTCGGCC TTCAAGGCCT ACTCTTCTTG GCATATTATT TTCCTGAATT GCTGCCTCTG      60
TTGTTCAAAC CATCCCGGAT TAATGACAAA AACTATCTT ATTCAAACCA AGAATTATCT      120
ACAACCTCC TTCTCAACTA GTTNNNGCAA GATCATTTCA GTTTTCTTT TTGTGCTACA      180
TCCTGGATTA ATTCTTCAGT TTNGTCTTCT CTGGAATCAC TACCTAAGGC TTATTCCATG      240
TTTCAAGTTT TTTGTTTTTT GTTTTTTTT ACTTTGATGA GTATGTTTAC CAACGCTCTC      300
GAG                                                                                   303
```

(2) INFORMATION FOR SEQ ID NO:358:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 493 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

```
GAATTCGGCC TTCATGGCCT ACAAAGTGTT GGAATTACAG GCGTGAACCTA CCGTGCCCAG      60
CCTTTTTTTT CATAGCAGTT TTATTAAGTT GTATTTGCCA TACCACCCAA TGTATCCATT      120
TAAGCACCTG ATTCAGTGGT TTTTCATGTA CTCATGGAGT TATGCAGCCA CAATCTTAGC      180
GCATTTTCAT TACCCAGAA AGAAACTGTA CCCATTATGC ACCCGGTTCC CNTCNTCCGG      240
TCNTGGCAAC CACGAGTGTA CTGTCTGTCT TCATGGATT TGCCTATTCTC GACGTTTCAT      300
TGGGATGAAA TCACACAGTG TATGGCTTCC AACTTTACT GTGCTGTTGT CAAGGTTTAT      360
CTATGTGTTG GGTGCAGCCA CCCCTTGGTA TCCACAGGGA TTGGACCCAG GAGCCTGCAC      420
CGATCCCCCTG CAGGGATGCC TGTGTCCAC AGTGCCCCCT GCAAACTCA CTGATATGAA      480
GAGTCGGCTC GAG                                                                                   493
```

(2) INFORMATION FOR SEQ ID NO:359:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 420 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

```
GAATTCGGCC TTCATGGCCT AGTTAACATG ACACAAAATC TTTACCTGCA GTTCTAATAT      60
TTTGCAAGGC TGAAGTCCAT ATTTACAAC GTCTTAGATC ATCTCAATCT GATTATTTAA      120
CTATTCTCTC TAACTGCTAG TCCAGCCCCCT AAAACTGCAT TTCTCTGCTC CTCCAAAGCT      180
TAGTGGCTTA TTGAAGTCCA TATTTGCATT GTGACAGAGC CAACTCCCA GAATGGATTG      240
CCACTCAGTG TAATGCAATA GGAGCACTTT AATTTATCT CCATTTCTG GACCCAGTGC      300
ATCATTCTAG CCTTTTTTTC TTGGAATGAA GTCTGGCTGA GAATGATGAT CCATTAGTAA      360
GAATTACTTA ATAAATCAAC TCTTGTTTAT GAGTGGCAGA AACTAAAGC CAGGCTCGAG      420
```

## (2) INFORMATION FOR SEQ ID NO:360:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

```

GAATTCGGCC TTCATGGCCT AATGTCACCA CTGTGGAAAA CCATATAGGT CGAAGGCTGG      60
ACTTGCATAT CACCTGAGGT CAGAGCATGG GCCTATATCC TTCTTTCCAG AGTCAGGACA      120
GCCAGAGTGC TTAAGGAGA TGAACCTAGA GTCAAAGAGT GGGGGCCGAG TTCAGAGACG      180
TTCTGCCAAG ATAGCTGTAT ACCACCTACA GGAGCTGGCC TCTGCTGAAC TGGCCAAGGA      240
ATGGCCCAAG AGGAAGGTGC TTCAGGACCT GGTACCTGAT GATCGAAAGT TAAAATATAC      300
TCGTCCAGGG CTCCCTACCT TCAGCCAGGA AGTACTACAT AAATGGAAGA CTCGAG      356

```

## (2) INFORMATION FOR SEQ ID NO:361:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

```

GAATTCGGCC TTCATGGCCT ACATGATGAA ATGTTGGCTA AAAGAGTCAC CCTAATATTA      60
ATAAAATGTT TTATTCTTCA TGTGACTAAA TCAGTGTGCA TGCAAGAAAA AGAAAGAAAA      120
AATGCTTAGA TTCCTTTTTT AAATTATCTC CAGAATTCTT AATTTTTATA AATTAAGGAC      180
CAACAAATCC CATTTTGTTT TCACGTTTGA CATTTGTTC TTTGACTTAA ATAACCTCTC      240
CACTCTTTAT TTTCTATTT GTGGTGATTT GAATAATTTT TCAGAAAAATA TGTACTTTCT      300
GATAAATTGT AGTGTGTGAG TAATGAAAAC TGCTCTATGG TGCTCCCCTC GAG      353

```

## (2) INFORMATION FOR SEQ ID NO:362:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

```

GAATTCGGCC TTCATGGCCT ACGAACTACT CTAAGTAATG GGCCAAGTCA TGAGCTGCAC      60
AAAGGCCCCC AAGACCCAGA CGGGTTTAAT GTTAAGCAAA ATGCCGCCTG GTCTCAGGTA      120
GACACTCAGC CACCGCTAGC CCCAGTCAAC TGTCCTATGG GAAGGCAGAA GGCCCGGTGT      180
TGCCAGGTCT TAAGTTTCA GGAGGAAATC CTTAAACGAT GGTGTTTCAC TATAATGGAT      240
TCATTTTTAT GTTTTATAAA TCTCTATGTT CATGTACTGG TATTAGTACT TTTATGTGAT      300
AAAATCTTTT TTTTAAACAT TGGTAATCA AAAACACAAC ACCCACATAC AGTGAGGACC      360
AAACAAAACC CGTCTGCAAG CAGGCTCTCT CCGAG      395

```

## (2) INFORMATION FOR SEQ ID NO:363:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 281 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

```
GAATTCGGCC AAAGAGGCTT ACAAAGGACA GCCCTGTCTG CACACTGAGT TACTGTGGAT    60
TTTAAAGAAA CTTGCTTAAA GAATTTAGGC ATTCTGATT CAGTTAAAGG ATTGCCAATT    120
CATCAGTCCC TGAAACTAGA GCAATCTCAA CAGGACAAGA AAAGAAAATG GGCTTTTAA    180
GTCCAATATA TGTCTTTTTC TTCTGTTTGG GAGTTAGAGT ATACTGCCAA TATGAAGCTT    240
ACCGATGGGA TGACGATTAT GACCAAGAGC AAAATGTCTGA G                    281
```

(2) INFORMATION FOR SEQ ID NO:364:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 357 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

```
GAATTCGGCC TTCATGGCCT AGTGCCACTG CACTCCAGCC TGGTGACAGA GTGAGNCTCC    60
GTCTCAAAAA AAAAAAAAAA AACTCAGCTT CTTGAGAGAG ATAAAATTGG GGGAGGAGCC    120
CAGGGCCACA TACCAAGCTT TGGGACATGG TGCCTCATGC TCTCTGGGAT TGCAGACCAT    180
CCAGGTCTGT CTTGCCCCCT GTTACTGCAC ATATATCCAC TCACATGTCT TCCCTCAGGC    240
TATCGGGCAG GGGGACTTCA CCAGGGGGTT TATGGATAGG CTCAAGAGG GTCTGTGAGC    300
CCCCAGAAAT TGTGTGTGAG ACTGAGTATG TGTTCTTTT TCCAGGAAAT TCTCGAG    357
```

(2) INFORMATION FOR SEQ ID NO:365:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 325 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

```
GAATTCGGCC TTCATGGCCT ATTACAATAT GCTTAAAGCT CAAAATGATC GAGAAACACA    60
AAGTTTGGAT GTCATATTTA CTGAAAGACA AGCGAAAGAA AAACAAATCA GAAGTGTCGA    120
AGAAGAAATT GAACAGGAAA AACAAGCAAC AGATGACATT ATCAAAAATA TGTCTTTTGA    180
AAACCAAGTC AAGTACCTAG AGATGAAAAC CACAAATGAG AAAGTGTAC AGGAATTAGA    240
TACACTTCAA CAACAATTGG ATTCACAGAA CATGAAAAAA GAGAGCCTGG AAGCAGAAAT    300
AGCTCACTCC CAGGTGAAAC TCGAG                    325
```

(2) INFORMATION FOR SEQ ID NO:366:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 549 base pairs  
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

```
GAATTCGGCC TTCATGGCCT AGTGAATTGA GTTTGTAAA CCTCCTTAGC ATATCACACA    60
ACACTAATTT TCCACTCTCA ATATGTGGCT GTAGAGTGTT TAATGTTTAC TTTCATATCG    120
CTTTTCCATA GTAGTGCAAG ACCTCAGTTT AGCTTGTTTA CATTATTGTC AGATTACTT    180
ACAGTGTAAT ATTTATTTCT GTTTTAAATA GTGTTTGCAA TAGGAGAAAA TCATATGATC    240
TTAAGCATAT ACACCAAAGG TAAGAAAGGA AGCCACTATT GTATCTTTT GATGAATTCC    300
AGATGAGCTG GGATCAAATT GAACTGCTTA GGCAGAAATT TAAGAGACAA GTAGAAGTGG    360
TGCAGAAAGA CATTGTGACT GCAATGTCCT ATTTACAGCT ACTGCCCAGA GGAGAACT    420
CCCAACATGA CAAAGAGTTC ATCAGCTTGA ATGTTAACTT TTGAAAACAA TTAATGAGC    480
CACTGCACCC GGCCAATCTA GTGAATTGAG TTTGTAAAC CTCCTTAGCA TATCACACAA    540
CTACTCGAG                                     549
```

(2) INFORMATION FOR SEQ ID NO:367:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 481 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

```
GAATTCGGCC TTCATGGCCT AGGAGGCGGA GGTGTCAGTG AGCCGAGATC ACGCCATTGC    60
ACTCCAGCCT GGGCGACAAC AGCAAGACTC CATCTCAAAA AAAAAAAGTG AGATCCTGCC    120
GATGGGCCCCT TCCTGTCCAC CTGTCAGGAA AACCTGCAAA AGGTTCTTGT CGCACCATTA    180
GAGCCAGTTT TTCCCAAATG ACACCCATAC CTGATTTTCC TTGTTCTTCT AAGACAGTTT    240
TAATTAGGAT AATCTCATAA GTGCTACATT TTCAGTGAAT TTTTCAATAT AGTGGCCCAT    300
GTTCTTTCTT TTTTTTTAAA GTCTTTTTC TCTGGTAGCA CATGTGATTT AATGCTTGCT    360
TTCTGAATT GTAGAAATAA AAGGAAATCA CAAGTATTTT CCAACAAAGT GGAAGTGGG    420
CCGAAGGGTG CAGAAAAAAA CTATAGAAAT TAGTTAAAAA TTAGGAAGGG GCAGTCTCGA    480
G                                     481
```

(2) INFORMATION FOR SEQ ID NO:368:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 285 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

```
GAATTCGGCC TTCATGGCCT ACCAACTCAG AAGGGAATGG AATGTGGAAA AAAAGAAAGA    60
AAACCTGAGT AACTTTTCCT AAAAAAGTCT AGCTGTTCTC AGTTTGTGGC ACCAAATGGG    120
GAGCAGGGAA TGTTCCAGTC GCAACTGACT AATTAGCCCA ACCCTNATTT ATTGATAATA    180
ATAATGATAA ATAATAATGC TAGCTAACAC TTAGTGAGCA AATACTAGGT ATTATGTGAA    240
ATCATTTCCT TGTATTAAT CACTTAATCT ACACAGCAAC TCGAG                                     285
```

(2) INFORMATION FOR SEQ ID NO:369:



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

```

GAATTGGCCT TCATGGCCTA NGTGTGGATA GTGGAGGCAT TGGTAGCCAG AACATGTCAC      60
TTTATGACAG CATATGGACA GCAATATGGA AGCCCAGCAT GGTGGTAAA AAATGGGGCA      120
GCCTAAGGTC AATGACTTTT GGCTGAGTCT GTGAAGATCT CAAAGCTTGG TGGTTTTTAG      180
CATAGCCTTT ATACCATACT TAACTCCGGG TAAGGACCAG GACCACTGTA GCGACCAATT      240
GATGACAGA GTAAAGTATG TGGGTTTTTT TTTTCCCCCA ACTGGGCTGA TTCTCTTAGA      300
ATAAAATTG TATACCATTA TATTATGTTA ACTTGATCAC AAAGAACAAA ATGTTATTTA      360
TTAATAATAT AGCATTGTCA TCTGTTTGAT GAATTTTCTT GATTTAATGC TTGTTTAGAT      420
TCAGTAAGCC ATTTCAGGA ACTATAATAA ATGCTTCTTC CAACTTCTCG AG              472

```

## (2) INFORMATION FOR SEQ ID NO:370:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

```

GAATTCGGCC TTCATGGCCT ACGAGTGCCT GCTGGAATCG TTTACCCTNG TTAATTTTTA      60
TCATNTCCTC TTTATGAGCA TGATATGGCT TCAGCTGTTC CACTTTGATC CAGGCATGAT      120
CTTCTGTTCC AAAAAATTTC ACAAAGAAGC ATTTCTTTCC GCGAGGTTTC TTCAAGTCCT      180
TTGGTGGATT AACAATCTTT CCTGGCCAAG GAGGATATCG GCCGAGTTTC CCCACACCA      240
AGTCGCCGAG CCGCAGACTC ACAGCCGCCA TCTTACCACC CAACCACCGC CGACGCACGG      300
GCCGCCG                                           307

```

## (2) INFORMATION FOR SEQ ID NO:371:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

```

GAATTCGGCC TTCATGGCCT ACAACGATCT TGTCTTCTTC TATCAGGTTT GCGAAGGTGT      60
TGCGAAGGCC AGCCATGCCT CCCACACAGC TGCCAGGCT GGGCTTCCTG ACAAGCTTGT      120
GGCTCGTGGC AAGGAGGTCT CAGACTTGAT CCGCAGTGGA AAACCCATCA AGCCTGTCAA      180
GGATTTGCTA AAGAAGAACC AAATGGAAAA TTGCCAGACA TTAGTGGATA AGTTTATGAA      240
ACTGGATTG GAAGATCCTA ACCTGGACTT GAACGTTTTT ATGAGCCAGG AAGTGCTGCC      300
TGCTGCCACC AGCATCCTCT GAGAGTCCTT CCAGTGTCTT CCCCAGCCTC CTGAGACTCC      360
GGTGGGCTGC CATGCCCTCT TTGTTTCCTT ATCTCCCTCA GACGCAAACT CGAG              414

```

## (2) INFORMATION FOR SEQ ID NO:372:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

```

GAATTCGGCC AAAGAGGCCT ACTGGATGGC ATCTACTTCG TATGACTATT GCAGAGTGCC      60
CATGGAAGAC GGGGATAAGC GCTGTAAGCT TCTGCTGGGG ATAGGAATTC TGGTGCTCCT      120
GANCATCGTG ATTCTGGGGG TGCCCTTGAT TATTTTCACC ATCAAGGCCA ACANCGAGGC      180
CTGCCGGGAC GGCCTTCGGG CANTGATGGA GTGTCGCAAT GTCACCCATT TCCTGCAACA      240
AGAGCTGACC GAGGCCCAGA AGGGTTTCA GGATGTGGAG GCCCAGGCCG CCACCTGCAA      300
CCACACTGTG ATGGCCCNAA TGGCTTCCCN GGATGCAGAG GAGGCCCAAG GACAAAAGNA      360
AGTGAGGNAG CTCGAG

```

## (2) INFORMATION FOR SEQ ID NO:373:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

```

GAATTCGGCC AAAGAGGTCC TGTAAGTATG ACTATTTAAT TTATTTCTTT TCACAATATA      60
AAAAGCACAT GCCATATTTT GAAAGACTAT TAAAGGTGGG GACAAGAGGT TATTTAAATC      120
TATGTTTGGA TGCAACTTTT ATGGCTTAAA CTACAAAGAA TTATCCTTTT TATATATTAA      180
ATGATTGTAT AGTTCTTTTA ATACTGTTTT TTGATACAAG TGTGAAATNC TTAAAGAAAA      240
TGGCAAACAT CACTAACAAAC CATTACAATT CTAATAGCTA ACTTTTCTGA GCCATTACTT      300
GGAACCATGC ACTGTTTAAA ATGCCTCACT TGGCCAATGC TCGAG

```

## (2) INFORMATION FOR SEQ ID NO:374:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

```

GAATTCGGCC AAAGAGGCCT AAAATGCGGA GTTATAATCC AGAAGGGGAG TCTTCAGGGA      60
GATACCGAGA AGTAAGGGAT GAAGATGACG ATTGGTCCTC TGATGAATTC TGAAGATAAT      120
CTCCTAAATC ACTGACGTTG AGATGTCATC ATCTTACATC AGACTTTCTA ACTAGTATCA      180
AGATCAGTGT CAGATATTGT TGAGGGAAGT AATTTTATAA AGTTACACAA AGGTAGTTAT      240
AAAAAAGCC CAGTTGTCTT TTCAGAAAGT GACTTTCATG TGCTTGAAAA GTTTAATATT      300
TGAATATTGT GTTTAACCAC ATGGTATTAA AATTTTGCAA TATATTGTGT ATTGGTCTGA      360
TATTTTAGTA TATAGTAGAA CATACTTTTT TTTTCTTTAA GCCAAATGAA AAGAGGTAAC      420
TTTGCTTTTT TCCTTTTCTT TACCTATCAA ATAGCATTTA TTACATGTCT TTCAGTGAAA      480
TACTTAGTTG TTCCAGGCAC GCTCGAG

```

## (2) INFORMATION FOR SEQ ID NO:375:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

```

GGAACGAATA GAAGTGTGTTG TATCTGTGGG TTNGACACAC TACTGAATCA CAAAGTCTTT      60
GGAATAATTC TCAAAGCCA TCACTTTTAG CCCACTTTCT CATTCAATTA TGCTCTATTC      120
TTTTTCTAGC ATGTCTAGCA GAATCTCTT GAATCTTGC AGTGAATTGG TGCTCCTTAA      180
ATACCTGCTA TTTTGAATA GTTTTGACTT AAATACATTT TCCTTTTCTC CCAGTTGCAA      240
AATGTCAGGG CTGACAACCTG AAAGGGCTTC TGAAGATTGT CAGTGTTCTC ATATTCAGAT      300
AGGTAGCAAA GAATCTGACA CATTGGGTAT AATAAACCCA CTCGAG                      346

```

## (2) INFORMATION FOR SEQ ID NO:376:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

```

GAATTCGGCC TTCATGGCCT AGGATGAATG ACCTTAAAGA TCGAACATGA ATAAGAGACA      60
TCATTTACCC TCAAAGAAAC TAGAGTCTGA TTGGGCAGGG AGGAAAAGGT ATTAAAATTA      120
TGTCTTTCTG CATTGTGTGG ATTTGAAGTT TGTTTTTTGT TGTTAAGAGT CTTATTATTA      180
GGATAATGAC ACTGTTTTTT CTTTATTAAG TTA CTGTGTG GGCAGTTAAG ATGATTCTGG      240
TGGCTCTTAA CATTTTTTTT TTCTCCAGTC GGAACATGC CCTGTGTGCC GCCGTCATTT      300
CCACCTGCG GTTATTGAAG CATCTGCAGC TCCTTCCTCT GAGCCTGATC CTGATGCCCC      360
ACGGTCTCGA G                                     371

```

## (2) INFORMATION FOR SEQ ID NO:377:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

```

GAATTCGGCC AAAGAGGCCT AGGAACTGTT CTGTTGAAAA TACCCATCCA ACAGTTTCTT      60
ACTATGCTCA TCCCCAAGTG GCATCCTACA ATACCTACTA CCATAGCCCT CCTCACCTGC      120
CACCATATTC TGCTTATGAC TTTCAGCATT CCGGTGTCTT TCCATCCTCC CCTCCCTCTG      180
GACTTTCTGA TGAGCCCCAG TCTGCCTCTC CCTCACCCAG CTACATGTGG TCCTCAAGTG      240
CACCGCCCAA AACTCGAG                                258

```

## (2) INFORMATION FOR SEQ ID NO:378:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 436 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

GAATTCGGCC AAAGNGGCCT AATATAACTT AGCTGCTATT TACAACACTA GAAATTTAGT	60
ACTTTAAGTA ATTTACATC TATGATAACA TTTGTTACTT TATTTTAAAT GATTTTTTTA	120
CAGTAGTTAT GACAGTAGGA TGGTTATGGA ATTGGAATTT AAACCTCCAA CTAATGAGCT	180
TAAGCTGCTT GGAATATTAA TTATGTAGTT TTTACATTCC ATTTTAAAC AAAAAGCTAG	240
NAAAGGTGCT GGCATTCTGA GGCCTGCAAT TAGGCCACAT AGCAGAAGCT TGCTCCTTCC	300
TTATCTGGGT GAAATATTTT ATTTTTCAC TTTGAGTCAT ATTCCCACCC CTGTATAAGC	360
TACATAGGAG CCTGAATGAA TTGGGTAGGA AAGGAAATTA TGCAAACAAG TCTCAGCTAG	420
TGCTGAATGA CTCGAG	436

(2) INFORMATION FOR SEQ ID NO:379:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 535 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

GAATTCGGCC AAAGNNGCCT AGCACATGCG TCCCCGCAGT TGTCTCTTC TCCTTTCCAA	60
GTTCTGNCT CTAAGGAGAT GGAAGTATTC TAAATTTTC TACTTCTAAT TTTTACTATG	120
CAACCAGCAA AGCGGGGAAG GTTGCAAGGA AAATGTCCG GTCTTTCACA ACTAAGNNGG	180
AAATTACTTC TCCTATGTTT TTATTCAAGA GTTGTCTTTA AAAGTGCCTG CCGGCTTTCC	240
CTTTTAACTT TTAGGATTAT AGTTAAGGTT ATGGAAAGTA GTCATTCATT AGTTCAGTAC	300
GTTTCATATA GTTCTCTAAC ATAGAAGAAA ACTCAGTCAC CAGACAGTGA AGTCATTTAG	360
CAGTGGTTAT TGGAAGATAA TCCACAGTGA TGGTAATGGA ATACTGGAAA CNCATCCTAA	420
ATAATCTGTA ATTATTATTA TTATTATTTT GGGACAGNGC GAGGCTCCGT CTCCAAAAAT	480
AAATAAATAA AATAAATAA TAAATAAATA AATAAAGGAT GGTGCACGTC TCGAG	535

(2) INFORMATION FOR SEQ ID NO:380:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

GAATTCTAGN CTGCTCTCGN GTCGCACCCA TGTTCAATCG TTCCTTCCTT CCTTCCTACA	60
TTCTTTTTTT TTNCCTTCTT CTCAGGGTC TCACTCTGTC ACCCTGGCTC GAG	113

(2) INFORMATION FOR SEQ ID NO:381:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 660 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

```

GAATTCGGCC AAAGAGGCCT ACACACATCG TTCATGTACA TGATCGCCGG ACTCTGCATG      60
CTGAAGCTCT ACCACAAGCG GCACCCGGAC ATCNACGCCA GCGCCTACAG TGCCTACGCC      120
TGCCTGGCCA TTGTATCTT CTCTCTGTG CTGGGCGTGG TCTTTGGCAA AGGGAACACG      180
GCGTTCTGGA TCGTCTTCTC CATCATTAC ATCATGCCA CCCTGCTCCT CAGCACGCAG      240
CTCTATTACA TGGGCCGGTG GAAACTGGAC TCGGGGATCT TCCGCCGCAT CCTCCACGTG      300
CTCTACACAG ACTGCATCCG GCAGTGCAGC GGGCCGCTCT ACGTGGGACC CATGCTGCTG      360
CTGGTCATGG GCAACGTCA* CAACTGGTCG CTGGCTGCCT ATGGGCTTAT CATGCGCCCC      420
AATGATTTCG CTTCTACTT GTTGCCATT GGCATCTGCA ACCTGCTCCT TTACTTCGCC      480
TTCTACATCA TCATGAAGCT CCGGAGTGGG GAGAGGATCA AGCTCATCCC CCTGCTCTGC      540
ATCGTTTGCA CCTCCGTGGT CTGGGGCTTC GCGCTCTTCT TCTTCTTCCA GGGACTCAGC      600
ACCTGGCAGA AAACCCCTGC AGAGTCGAGG GAGACAACC GGGACTGCAT ACCCCTCGAG      660

```

(2) INFORMATION FOR SEQ ID NO:382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

```

GAATTCGGCC AAAGAGGCCT AGTGTGGGGA GCTGTGGGCT GTGCCCTTCC AGTCCCCCAG      60
AGCAGTGCCT TTGCCAAGA ATCTCCTAGC GAGAGACCAG GGGCTACTGC CAGGTGACAG      120
AAAAGGGGAA ATCAGTTCCG CTATACCCAC AGCTCACCTG GCGGCCTGGG GCCTGCACAG      180
GGCCTGGTTG AGGCAGTGGG CCCCATTTT GGGCCGTCTG TGGAGTTGAT GTTCTGCCA      240
GCTGGTCCCT CTCTGTCTTC CCTGGAATT CACCTGCAGT TTGATGCCTG AGTTAAAT      300
GTTCTTCTAA ATAATCACT GTAGACTTTC TGTTTTAGC TATGTGAAAA CTTCTGAGAA      360
ACTTGAGAG TCTCGAG                                     377

```

(2) INFORMATION FOR SEQ ID NO:383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

```

GAATTCGGCC TTCATGGCCT ACTGGGCGGT CTTTGACGCA ATAACAATAT CTGCTCCATC      60
CTTTGCTGCT TTCAATGCAA TAGCTTTGCC AATGCCACGG CTGACACCTG TGATAAAAAAC      120
TGTACATCCT GCCAGCCTCC CGGTGTTGGG TAACATGACT TTCGTAGATC AGAGGAGGCG      180
GCGGGCGAAG CGCACGTCGA GCGGGGAGC GCGCTGCCT GTGGAGATCC GCGGAGGCCG      240
ACAGGATTCG TTGGCTGCCG TCCCCGCTGC TGTGCATTGG GTTAAAAACG ACAACCAACT      300
CGAG                                     304

```

## (2) INFORMATION FOR SEQ ID NO:384:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

```

GAATTCGGCC AAAGAGGCCT ACTTATTTTA CACAGCTTGA TTAAGGTCTA TGTCGGTATA      60
ATTTTTTTTA TGAGTCTNAC ACGTGGGATT TGTGAGCTT CTTGAATTTG TATGTTTATA      120
CAAATTTAGG AATTTTTTTC ATCCATTATT TATTTGAATA TATTCTCTGT CTTCAGTGTC      180
CTTTGAGGAC TCCAATTACG CATATACCTA ATTGCCTGGA GTTGTCCCAT AGCTTACTGA      240
TGCTTTGTTT ATTTTTTTCT TTCTTTTCTT CTCACCATGC TTTAGTTAGG ATAGTTTTTA      300
T TACTGTTTT TTTAAGTTTG CTAATCTTTT CTTCAGCAT GCCAGCTCGA G                351

```

## (2) INFORMATION FOR SEQ ID NO:385:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

```

GAATTCGGCC AAAGAGGCCT AGCGTCTTGG ACATGCCAGG AATAAAAAGG ATACTCACTG      60
TTACCATCTT GGCTCTCTGT CTTCGAAGCC CTGGGAATGC ACAGGCACAG TGCACGAATG      120
GCTTTGACCT GGATCGCCAG TCAGGACAGT GTTTAGATAT TGATGAATGC CGAACCATCC      180
CCGAGGCCTG CCGAGGAGAC ATGATGTGTG TTAACCAAAA TGGCGGGTAT TTATGCATTG      240
CCCGGACAAA CCTGTGTAT CGAGGGCCCT ACTCGAACCC CTACTCGACC CCCTACTCAG      300
GTCCGTACCC AGCAGCTGCC CCACCACTCT CAGCTCCAAA CTATCCCACA TATCTCGAG      359

```

## (2) INFORMATION FOR SEQ ID NO:386:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

```

GAATTCGGCC AAAGAGGCCT ACTACATGTA AAACACTTTT ATTCATTAAA AAGAAAACCTG      60
ACTGGCTTGG ACCTACAAAT TAGTTTCATT ATTTGTTAAT GTTGAAAGC CATTAAAAGA      120
TGAATATATA GGTTTCTTTA TACTCAATAC TTGTAGTTTT GTTTGGGGGA ATGAGAGGAT      180
GCCCTTGATA CCTTTGTGAG GCCTCTCCAC TGAGGGTCAA TCATGACTTC TGTTTTAAAC      240
CAGCCCATCC CATCTTCTCC AGCTGCTCTC CTTATGTCTT GCTTCTCTCC CCTCCACCT      300
TCTCAGCACC AGGACTCGAG

```

## (2) INFORMATION FOR SEQ ID NO:387:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

```

GAATTCGGCC TTCATGGCCT AGTGGGAGCT ATTTTCTTTT TTGTGCATAT AGATATTTCT      60
TAAATGAAGC TGCTTTCTTG TCTTTTATTT CTAAAAGCCC CCTTATACCC CACTTTGTGC      120
AGCAAAGATC CCCGTGCAGG TCACAGCCTG ATTTGTGGCC AGGCTGGACA AATTCCTGAG      180
GCACAACCTG GCTTCAGTTC AGATTTCAGG CTGTGTTGGT GTTGGGACCA GCAGAAGGCA      240
AACGTCCAGC CAACACACAG GACTGCAAGA GGTCTCGAG                               279

```

## (2) INFORMATION FOR SEQ ID NO:388:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

```

GGTAGAAGCA GGAGGTTTTC AACCTAGTCA CAGAGCAGCA CCTACCCCTT CCTCCTTTCC      60
ACACCTGCAA ACTCTTTTAC TTGGGCTGAA TATTTAGTGT AATTACATCT CAGCTTTGAG      120
GGCTCCTGTG GCAAATCCC GGATTAAAAG GTTCCCTGGT TGTNAAAATA CATGAGATAA      180
ATCATGAAGG CCACTATCAT CTCCTTCTG CTTGCACAAG TTTCCTGGGC TGGACCGTTT      240
CAACAGAGGC TCGAG                               255

```

## (2) INFORMATION FOR SEQ ID NO:389:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

```

GAATTCGGCC TTCATGGCCT AGGCCCACAT AGAAGAAATG AATGAAAAGA CTTTAGAAAA      60
GCTTGATGTG AAGCAAACAG AACTAGAATC ATTATCTTCT GAACTGTCAG AAGTATTAAA      120
AGCCCGTCAC AACTAGAAG AGGAACTTTC TGTTCTGAAA GATCAAAACAG ATAAAATGAA      180
GCAGGAATTA GAGGCCAAGA TGGATGAACA GAAAAATCAT CACCAGCAGC AAGTTGACAG      240
TATCATTAAG GAACACGAGG TATCTATCAA GAGGAACTCG AG                               282

```

## (2) INFORMATION FOR SEQ ID NO:390:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

GAATTCGGCC	TTCATGGCCT	AGATAGAGCT	CAAAAACATG	GCATGGATGA	ATTTATCTCT	60
TCCAACCCCT	GTAACCTTGA	CCACGCTTCC	CTCTTTGAGA	TGGTACAACG	CCTTACTTTG	120
GATCACAGAC	TTAATGATTG	CTATTCTTGC	CTGGGCTGGT	TCAGTCCTGG	CCAGGTGTTT	180
GTAAGTAGAC	AGTATTGCGC	CCGAAATGGA	GTCCGGGGGT	GTCACCGACA	TCTCTGTAC	240
CTCAGAGACT	TGCTTGAACG	GGCAGAAAAT	GGCGCCATGA	TCGACCCAC	CCTTCTTCAC	300
TACAGCTTTG	CCTTCTGTGC	ATCCCATGTC	CATGGGAACA	GTCAACAAAT	GCATGTGTAC	360
CTTAGTGGGC	TGCCACCAAA	TACAGACCAC	GGTTCTTCCC	TATAGTGAGT	CGTATTAATT	420
TCAGAGGAGT	ATTTAGAAGA	GAAGCTGAAG	CTGTCGAG			458

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

GAATGGGACT	CCAAGCCTGC	CTCCTAGGGC	TCTTGCCCT	CATCCTCTCT	GGCAAATGCA	60
GTTACAGCCC	GGAGCCAGAG	GAGCGGAGGA	CGCTGCCCC	AGGCTGGGTG	TCCCTGGGCC	120
GTGCGGACCC	TGAGGAAGAG	CTGAGTCTCA	CCTTGCCCT	GAGACAGCAG	AATGTGGAAA	180
GACTCTCGGA	GCTGGTGCAG	GCTGTGTCGG	ATCCCAGCTC	TCCTCAATAC	GGAAAAATACC	240
TGACCCTAGA	GAATGTGGCT	GATCTGGTGA	GGCCATCCCC	ACTGACCCTC	CACCTCGAGG	300
TTCTCCCTAT	AGTGAGTCGT	ATTAATTTTC	AGAGGAGTAT	TTAGAAGAGA	AGCTGAAGCT	360
GTGCGAG						366

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

GGCGGGTGGG	GGTTAATTAT	CTGAAACCTA	CTAAAACGGA	CTACAGTTAT	CTCTAGGCCAA	60
TGCTGTTGGA	GTGTTTCCTG	CAAATGCATT	TCACTCATTT	TTTGTGATT	ATTTTATAAG	120
TATACTGGGG	CAAAAATTTT	ACATTCTAAA	TTGTTCTTAT	TTATTATTTT	TATTATAGAT	180
ATATGAGGAT	ATTACTTACT	CTATTACACA	TATAATTTAT	CTTTTAAATT	TTCAAGTGAG	240
TTCTACAATT	AACTTTATCA	TCTAAATTCT	CATTACAGAT	AGCATTTTAA	TGTCCAGAAA	300
GAAAAAAGG	TTTTTTATTG	TTATATGTGA	AACCATAAAA	ATATTACCAG	CTTGTGGCCG	360
GGCGTGGTGG	CTCAGCCTTA	TAATCCCAGC	ACTTTGGGAG	GCCGAATCAC	CTGAGGTCAG	420
GAGTTCAAGA	CCAGCCTGGC	CAACATGCGG	AAACCCCGTC	TCTACAAAAA	TGGAAAAATT	480
AGCCCGGCAT	GATGGCAGGT	GCCTGTAATC	CCAGCTACTC	GAG		523

(2) INFORMATION FOR SEQ ID NO:393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 548 base pairs



(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

GAATTCGGCC TTCATGGCCT ACCCAGATGA AACTTTTGGG GGGAGAGTGC CCAGACCAGC	60
CTTTGTCCAC TATGACAAGG AGGAGGCATC TGATGTGGAG ATCTCCTTGG AAAGTGACTC	120
TGATGACAGC GTGGTGATCG TGCCCGAGGG GCTTCCCCC CTGCCACCCC CACCACCCTC	180
AGGTGCCACA CCACCCCTA TAGCCCCAC TGGGCCACCA ACAGCCTCCC CTCCTGTGCC	240
AGCGAAGGAG GAGCCTGAAG AACTTCCTGC AGCCCCAGGG CCTCTCCCGC CACCCCCACC	300
TCCGCCGCCG CCTGTTCTTG GTCCTGTGAC GCTCCCTCCA CCCCAGTTGG TCCCTGAAGG	360
GACTCCTGGT GGGGGAGGAC CCCCAGCCCT GGAAGAGGAT TTGACAGTTA TTAATATCAA	420
CAGCAGTGAT GAAGAGGAGG AGGAAGAGGA AGAAGAGGAA GAAGAAGAAG AGGAAGAAGA	480
GGAAGAGGAG GAAGACTTTG AGGAAGAGGA AGAGGATGAA GAGGAATATT TTGAAGGGGT	540
TACTCGAG	548

(2) INFORMATION FOR SEQ ID NO:394:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 577 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

GAATTCGGCC TTCATGGCCT ACTTACTAGG AATTAAAAGA CGGATTTCCA AGGAGATTCA	60
GAGGCAGCAA GCACTACAGA AGTCAGAACT CCAGCACCAT CTGCTCCGTT TCTTGAAGTT	120
TGCTGAACGA GGAATCACAG CTGCAACGTG GGGTGATTGT ATTGATCAAA ACCCACTGGG	180
AAGSACAAAG AGTTTGCCGC CTTTCGGGGA TCCAAGGGAC TGTGGCGACC GTGCCTCTGT	240
GCCAGCGTCC CAGGAAGGAA GCCAACCCTG AGCGAGCCTG TCCTCTGTGG CAGGTCCACA	300
CGGTGTGGGT GGGCAGGGCT TGGACCCCG TCTCCATGGC AGGTCCATAC AGCATGGGTG	360
GCAGGGTTTG GACCCGCCCA GCAGCACCAC GGACCCAGC CACTCTCGGG GGCAGACGTC	420
AGAATCCGTT CCGGAGCAGC TCCCGTGCCC TGGGGGCAGT CACAGAGCCC CCCAACACCC	480
CCGTGCTCTG CACGAGCCTC TCCCTCCACA CCCGAAGCAG GCGTCCATCT GTGTCCTCCT	540
GGCAGCCCCT CAAACACACA CCACCCATA TCTCGAG	577

(2) INFORMATION FOR SEQ ID NO:395:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 415 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

GAATTCGGCC TTCATGGCCT ACATCTTCAT TGCTGAGGTT GCAGCTGCTG TGGTCGCCTT	60
GGTGTAACAC ACAATGGCTG AGCACTTCCT GACGTTGCTG GTAGTGCTCG CCATCAAGAA	120
AGATTATGGT TCCCAGGAAG ACTTCACTCA AGTGTTGGAAC ACCACCATGA AAGGGCTCAA	180
GTGCTGTGGC TTCACCAACT ATACGGATTG TGAGGACTCA CCCTACTTCA AAGAGAACAG	240
TGCCTTTCCC CCATTCTGTT GCAATGACAA CGTCACCAAC ACAGCCAATG AAACCTGCAC	300

CAAGCAAAAG GCTCACGACC AAAAAGTAGA GGGTTGCTTC AATCAGCTTT TGTATGACAT 360  
CCGAACTAAT GCAGTCACCG TGGGTGGTGT GGCAGTGGA ATTGGGGGCC TCGAG 415

## (2) INFORMATION FOR SEQ ID NO:396:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

GAATTCGGCC TTCATGGCCT ACTAAAAGAT ACTTCAAAGT GACAAAAACG TGTCCTTCC 60  
CCACTTAGAG ACAATGATTA ACAGGGCCCT ATATGTTCTT ACCACATACA GAGGATGCAT 120  
TTATTTTTCG TCTATGACAC TTGCAAAAAT CTCTACTGTA ATTAATTTGG GTCTATTATT 180  
AACTCTCTGT TCCATCATAG AATGTGGCCA GGCCTTACAA TGGAGAGCCA GAGTTAAAC 240  
TTCAAGTTGC ATCTGTTTTT GGGCTGAGTC ACCACCGGAC CTCGAG 286

## (2) INFORMATION FOR SEQ ID NO:397:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

GAATTCGGCC AAAGAGGCCT AAAAATGAAA ACCTCTGCAC TTTAATTTTT TTCAGTAATT 60  
TCCAGCTATT TCTAGGTATA AAGAGCAGCT CGTTCTCTT ATTTATTTTA GTCTCATGTG 120  
TCAATACTTT CCGATGCTTT GCTTAATTCA TGTATGTGTG CAGTGCTGCA ATGCCCAGAC 180  
AAACGTGAGC ACACCCACCA ATCTCGAG 208

## (2) INFORMATION FOR SEQ ID NO:398:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

GAATTCGGCC AAAGAGGCCT ATGATGAAGC TGGGCATTTA TAACTAGATT CATTAAAGGAA 60  
TACAAAGAAA ATACTTAAAG GGATCAATAA TGGTGTCTTC TGTTGCAGA ATGCGAAGTC 120  
TGTGGTTTAT CATTGTAATC AGCTTCTTAC CAAATACAGA AGGTTTCAGC AGAGCAGCTT 180  
TACCATTTGG GCTGGTGAGG CGAGAATTAT CCTGTGAAGG TTATCTATA GATCTGCGAT 240  
GCCCGGGCAG TGATGTCATC ATGATTGAGA GCCTAACTA TGGTCGGACG GATGACAAGA 300  
TTTGTGATGC TGACCCATTT CAGATGGAGA ATACAGACTG CTACCTCCCC GATGCCTTCA 360  
AAATTATGAC TCAAAGGTGC AACAATCGAA CACAGTGTAT AGTAGTTACT GGGTCAGATG 420  
TGTTTCCTGA TCCATGTCCT GGAACGCTCG AG 452

## (2) INFORMATION FOR SEQ ID NO:399:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

```

GAATTCGGCC AAAGAGGCCT ATCTTCCTGA AGAGCAATGG AGCCGCTTTT ACTTGAAGA      60
GGACTAATCG TATATCTAAT GTTCCTCCTG TTAATAATTCT CAAAAGCAAT TGAAATACCA      120
TCTTCAGTTC AACAGGTTCC AACAAATCATA AAACAGTCAA AAGTCCAAGT TGCCTTTCCC      180
TTCGATGAGT ATTTTCAAAT TGAATGTGAA GCTAAAGGAA ATCCAGAACC AACATTTTCG      240
TGGACTAAGG ATGGCAACCC TTTTATTTC ACTGACCATC GGATAATTCC ATCGAACAAT      300
TCAGGAACAT TCAGGATTCA CAACTCGAG                                     330

```

## (2) INFORMATION FOR SEQ ID NO:400:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

```

GAATTCGGCC TTCATGGCCT AAGCAAACCC AGAGGTGGAT GTTATGAACA GCTGTGTCTG      60
CCAAACACAT TTACCCCTTG GCCCCTTTT GAAGGGCAAG AAATGGCGTC TGCTCTGGTG      120
GCTTAAGTGA GCAGAACAGG TAGTATTACA CCACCGGCC CCTCCCCCA GACTCTTTT      180
TTGAGTGACA GCTTCTGGG ATGTCACAGT CCAACCAGAA ACACCCCTCT GTCTAGGACT      240
GCAGTGTGGA GTTCACCTTG GAAGGGCGTT CTAGGTAGGA AGAGCCCGCA GGGCCATGCA      300
GACCTCATGC CCAGCTCTCT GACGCTTGTG ACAGTGCCCTC TTCCAGTGAA CATTCCCAGC      360
CCAGCCCCAT CCTCGAG                                     377

```

## (2) INFORMATION FOR SEQ ID NO:401:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

```

GAATTCGGCC TTCATGGCCT AGGCAAGGTC TTCGGCTCGT GCCGTTCTAA GCCGGAGAAT      60
TCTCGCGGGA GCAGGGTTAC GTCCTCGTGG GATTCGTTGG CGGTGGCTGA GGTCTCCAG      120
CAGCCTGACC TGAGTGGGTT AGTGATCCAG AGAAACCAGC AGGCCAACTT GGTGAGGAAG      180
GTTTCGGGAAG CTGTTGGAGC AGTGTGGGGA ATTTCCACC AGGATGAGTA TGATTGGCTG      240
TGATTTTAGA TCGTAAAGCT GAAAATTGAA ATCATGAAAG TAGACAGGAC TAACTGAAG      300
AAGAACTCGA G                                     311

```

## (2) INFORMATION FOR SEQ ID NO:402:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 357 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

GCATTGATGG AAAAGCATAA TGTCTTAGAA AAAGGCTTTC TAAAAGAAAA AGAGCAAGAG	60
GCCATTTCTT TTCAAGATAG ATACAAAGAA CTTCAGGAAA AACATAAACA AGAATTGGAA	120
GACATGAGGA AAGCTGGTCA CGAAGCCCTC AGCATTATTG TGGATGAATA TAAGGCACTA	180
CTGCAGTCTT CAGTTAAGCA ACAAGTAGAA GCTATTGAAA AACAGTACAT TTCTGCAATT	240
GAGAAACAGG CACACAAGTG TGAGGAGTTG CTAATGCTC AGCATCAGAG GCTCCTTGAA	300
GTGCTAGATA CAGAGAAGGA ACTGTAAAA GAAAAATAA AGGAAGCCCA TCTCGAG	357

(2) INFORMATION FOR SEQ ID NO:403:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 492 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

GTTCTAGACC TGCCTCGAGC GTTAATGGTA TAAATCACTT GTTTGTAAAG TATTGTTTTT	60
AAATATTGCC AGATTGATA TCTTAGTATT GTATTTTAT ATTTGTCTTC ATGTGTTTTT	120
GTTTTCTCAT AAGTGTCTGT ACCCCCCTTT TTTTTCCTT AAAGAGAAAT AATGAGAGAG	180
ATTGTCTGTC TTGAAGTTCT CAGTGCCTGT GCATTGCTGC CACTACACAG CTAGTATCAT	240
GACAGCAGCT TCAGAACCAG AGCTGGCTTC CAGGCAAGGC TGGGTGGGGA AGAAAGAGAA	300
AAACAAAAGA ATTATTTCTC TATGCCGAGA CCAGCTCGGT CAGGGAGACC CTAACCTAGC	360
GGTGCTAGAG GAATTAAAGA CATAGACACA GAAATATAGA GGTGTGAAGT GGGAAATCAG	420
GGGTCTCACA GCCTTCAGAG CTCAGCCACG AACAGAGATT TACCCACGTA TTTATTAACA	480
GCAAGACTCG AG	492

(2) INFORMATION FOR SEQ ID NO:404:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 395 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

GAATTCGGCC TTCATGGCCT ACTTCCCTCT AAGGTCCCCA AATGCCTCTC ACGTGCCTAG	60
CATTTAGCTG CTGCACCGAG CATGCTCACT GACAACTTT TGGCCAAGAA GAGCCTTTTG	120
GTCTCTCTTG GTCAGATCTA GGAGGCTTC AGGACTCTCC AAAACTCACC CACTCAGAGA	180
GCCTGCCAGG AACACTCAGC TGAGCGATGG CATTGTGGAG CCTGGGTTTT CAGAAGGGAG	240
CCCATAGTGA GTGGTAGCAT AACCTTGTTA AGGTTGTATT TTCCTTAGAT ATAGAAACAA	300
ATCAAATGCT GCTAAATTGG TAAGGGATGG AGTTTTATA TCACGTCACA TTTGCTGAG	360
CCGTAACCAG ACAGGGAAAA AGCAGAGACC TCGAG	395

## (2) INFORMATION FOR SEQ ID NO:405:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

```

GAATTCGGCC TTCATGGCCT ACCAAGTTCT AACTGTAAAA TGGGGACATT TTACCTTTCT      60
TTCTTTGGAT AGGATCAGTT CTTAAGAGCA GCCCGGTAA CTGGAGGAAT GGGAGCCGTT      120
TTGATGAGAA AAATGGGCTG GAGAGAAGGA GAAGGATTAG GAAAAACAA AGAAGGCAAT      180
AAGGAACCCA TCCTAGTTGA TTTAAGACA GACCGAAAAG GTCTTGTTC AGTAGGAGAA      240
AGAGCACAAA AGAGGCCTCG AG                                     262

```

## (2) INFORMATION FOR SEQ ID NO:406:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

```

GAATTCGGCC TTCATGGCCT ACCCATTTGT CAATTTTGC TTTGTTGCAA TTGCTTTTGG      60
TGCCTTTGTC ATGAAACCTT TGCCTACAGG TGCTGTTTAT TTACACCCCT GTCCCAACCT      120
CACCCCACTC CTTTTCTTTT GCTGGTGGGA AGTCAGTAAG AACTGTGGGT GGGGTTCTGA      180
GGTAATCAAT ACAAAGAAGA AGGTAAGAAA TTGGAGGGGA CTCAGGGGAG ATGGCAATGC      240
TGACAAGGGG TTGGATGGAA TTTGTTCTGT AAAC TGGAAG CAGCTCGAG                289

```

## (2) INFORMATION FOR SEQ ID NO:407:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

```

GCTCCTTCTG TATCCTTCCT TTCCCATCTG TCTGCTTCTA ACAAATAAGA CAAGCTAAGA      60
AGCAGCTTGT TTCATGATTC TATACTCACT TCCAAGCTTT CTCTGCATAG ACTTTCCTAG      120
TTTGCCACTT TATCTTTTCT CCATCCCTCC AGCCAGTCAT GAGATTCTAC TCCCCATTCA      180
TACATGCATT TATTATCCA GACTTTACTG AAGGCTTACT CTTTGAACCT TGCAAAATGC      240
CAGTGAGGCA AAGCATGCAT CCTGTACAGG AAAA ACTCAG TCTAGAGGGG AGAGATAAGC      300
AAACAAGTGA TTACCACACC AGGCTCGAG                                     329

```

## (2) INFORMATION FOR SEQ ID NO:408:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

ATTGAATTCT AGACCTGCCT CGAGAGCTTT TGAGATTGTC TATTTTGTCT GAGTGAGTTT	60
TGGTACTTTA TTGTTTTCGA TTGGTCCATT TCTTCTACGT TGTCAGATCT CTGAGTGTCA	120
AGTTGTTTCAT AGTACTCCGT TATTATCTTT TTCATGACTG TAGGATCTGT GGTGATATTG	180
ATGATTTGTG TCTTCACTCC TTTTGTGTGG CCTACACTCG AG	222

(2) INFORMATION FOR SEQ ID NO:409:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 505 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

GAATTCGGCC TTCATGGCCT AAACCTGCAG AAATGAAGAC TAGAGTACAC AGCACACTCA	60
GAGCCCAGAC AGACTTCGTC CCAGGACATC ATCTGTTCTT GATGCCCATT CTTCTCTCCT	120
AAACATCATT TACTTTTTCC TCTAAAAGTG CCTGCAGACC CCCACTACTC TCTCCCATGG	180
AGAAGGGCAT ATAAGCTTCG AATCTCACGG GGTATTGGG CACTCTGTCT CTTGTGATGC	240
TCCTATGCAT GTAATAAATT TATGTGCCTT TTCTCCTATT AATTGGTCTA ATGTCCATTT	300
ATTCCATAGA TTCAATTATC AAACCTCTCAG AGGGCAGAGG GAAAATTTTC ACTCCCTTAT	360
ATCATCAGAA ATATAAATAA AAATAGCACA ACACTCAGTA AATGATTATG TTATTATTGT	420
TATGTTTGTG ATATCTTGGT GTCTGGTTAT TTAAATCAT ATCACTTAAA GAAACAGTGT	480
TCCTTAGGCC ATGAAGGCCG AATTG	505

(2) INFORMATION FOR SEQ ID NO:410:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 650 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

GTATGAACAT TGAGGGCCCA GATCTCAATG TGGAAGGTCC GGAGGGAGGC TTGAAAGGTC	60
CCAAATTCAA GATGCCTGAC ATGAATATCA AAGCTCCCAA GATCTCCATG CCTGACATTG	120
ACTTAAACTT GAAAGGCCCC AAGGTGAAAG GTGATGTGGA TATTTCTCTT CCCAAACTTG	180
AAGGGGATCT GAAAGGGCCA GAGGTGATA TCAAAGGCCC TAAAGTGGAC ATCAATGCCC	240
CAGATGTGGA TGTTTCATGGT CCAGACTGGC ATCTGAAGAT GCCCAAAGTG AAAATGCCCC	300
AGTTCAGCAT GCCTGGCTTC AAAGGAGAAG GCCCTGAAGT CGATGTTACC CTCCTAAAG	360
CTGACATTGA CATTTCCTGGT CCCAATGTAG ACGTTGATGT TCCAGACGTG AATATTGAAG	420
GTCCAGATGC AAAGCTGAAG GGCCCAAGT TCAAGATGCC TGAGATGAAC ATCAAAGCCC	480
CCAAGATCTC CATGCCTGAC TTTGACCTGA ACTTGAAGGG ACCCAAATG AAGGGTGATG	540
TGGTTGTGTC TTTGCCCAA GTGGAAGGTG ATCTAAAAGG CCCTGAGGTG GACATCAAGG	600
GCCCCAAAGT GGACATTGAC ACTCCTGACA TTAACATCAA GAGGCTCGAG	650

## (2) INFORMATION FOR SEQ ID NO:411:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

```

GAATTCCGCC TTCATGGCCT AGGGGCTGGA GGGTGGCCCG AAGCAGATGG GGCCGGCCTT      60
GCAGGCACTT CTAAGGCCTT GGGGTTTGCT TCCGAGGGAG TAGGGAAGGA GAGCGATGTC      120
ACCTGTGAG GCTTGGTCAC ATACCCCAAT GGATTTGGTA GCACACGCCA CAGTGAAGGT      180
ATAAGCTACT GTCATCACAC GTAATTATTT CATGAAACAG AAAATTTTAA AATAAAAGAA      240
AATAGAAGTT TCCCTATTTT CTTCTCCTGC ACTATTGGAT CATCCTGTTT AGCCCTCTTT      300
TAAGACAAAT GGAAGTAGCA AACGAGTGTA AATAGGAATG AATGGTTTGT TGGGGTTTAT      360
TTATTTTAT TTTATTTTAT TTTATTTTAT TTTATTTTAT TTATTGAGAC AGAGTTTCAC      420
TCTTGTGCC CAGGCTGGGC TCGAG                                         445

```

## (2) INFORMATION FOR SEQ ID NO:412:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

```

GCCTGCCTCC AGGCCTTTGC TCCCACTGTT GNCTCCACTT AGAATAACAT TCCACCCCAT      60
CTCTATAAAT ATCCTACAGA CAAATACTAC CTTCCCCTTA AGGCCAGTTC TAACCCTAAC      120
TGACAACAAA TCATCTCTAC ATGATCTTTT CTTCTGCGGA ATGCCTGCAG CACTGTTTAA      180
TCCTGCCCCA CCACCATCCC CTCACCCAGC ACCCTCTCCC AGACCAGACA GGGTGGCTCA      240
TGCCCTGCAAT CCCAGCACCT TGGGAGGCTG AGGCAGGAGG ATTGCTCGAG      290

```

## (2) INFORMATION FOR SEQ ID NO:413:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

```

GAATTTGACA TCTTAGAACA TTCTGCAACC TTTTGCTGG GAAATGGAAA CAGATCTAAT      60
CTTTACCACC CTCATGGCTC AAGGACCTCA TCTGGCAGCC TGGCTCATGT TTTTCAGCCA      120
AGTAGCTTCC AGCTTACAGC AGCCCTCAAA TTTGGACCTG CCACCAGCTC CAGAGCTTGA      180
CTGGATGGAG ACAGGACCAT CTCTGACATT CATTGGCCAT CAGGATATAC CAGGAGTTGG      240
TAACATCCAC TCAGGTGCCA CACCTCCCTG GATGATCCAA GATGAAGAAT ACATTGCTGG      300
GAACCAAGAA ATAGGACCAT CCTATGAAGA ATTTCTTAAA GAAAAGGAAA AACAGAAGTT      360
GAAAAAATC CCCCAGACC GAGTTGGGGC CAACTTTGAT CACAGCTCCA AGGACCTCGA      420
G                                         421

```

## (2) INFORMATION FOR SEQ ID NO:414:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

GAATTCGGCC TTCATGGCCT AAGCCAGTCA ACCAGCAGTA TTAGTGCTGT TTTCAAAGAT	60
TTAAGCTCTA TAAAATTGGG AAATTATCTA AGATCATTTT CCCTAAGCAT TGACACATAG	120
CTTCATCTGA GGTGAGATAT GGCAGCTGTT TGTATCTGCA CTGTGCTCTGT CTACAAAAG	180
TGAAAAATAC AGTGTCTTACT TGAAATTTTA ACTTTGTAAC TGCAAGAATT CCAGTTCAGC	240
CGAGCCACTT CGAG	254

## (2) INFORMATION FOR SEQ ID NO:415:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

GCAAACAGAC AAGGCTTACA GGTTAGTTCA GGATCTGCGC CTTATCAAGC AAATTGTTTT	60
GCCTATCCAA CCTGCGGTGC CAAACCCATA TACTCTCCTA TCCTCAATAC CTCCCTCCAC	120
AACCCCTCCA TAACCCATTA TTCGGTTCTG GATCTCAAAC ATGCTTTCTT TGCTATTCTT	180
TTGCATCCTT CATCCCAGCC TCTCTTTGCT TTCACTTGGG CTGGCCCTGA CACCCATCAG	240
CCTCAGCAAC TTACCTGGGC TGTACTGCCA CAAGCCTTCA CGGACAGCCC CCATTACTTC	300
AGTAGCCCTC GAG	313

## (2) INFORMATION FOR SEQ ID NO:416:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

GCCTGCCCCC ACCTTACAGG TCTGGGATGT ACCTTTCCAT CTGTTGCTGC TTTCTTCTAT	60
GGGCCCCTGC CCTCACTCTC AAGAACCTCA ACTACTCCGT GCCGGAGGAG CAAGGGGGCCG	120
GCACGGTGAT CGGGAACATC GGCAGGGATG CTCGACTGCA GCCTGGGGCTT CCGCCTGCAG	180
AGCGCGGCGG CGGAGGGCGC AGCAAGTCGG GTAGCTACCG GGTGCTGGAG AACTCCGCAC	240
CGCACCTGCT GGACGTGGAC GCAGACAGCG GGCTCCTCTA CACCAAGCAG CGCATCGACC	300
CGGAGTCCCT GTGCCGCAC AATGCCAAGT GCCAGCTGTC CCTCGAG	347

## (2) INFORMATION FOR SEQ ID NO:417:

## (i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

```

GAATTCGGCC TTCATGGCCT AGCAGATGAT TGACATTGCT ATCGATGGTT TCCTTTTGAC      60
TCCAGTGCAG AAGATCTGCA AGTATCCCTT ACAGTTGGCT GAGCTCCTAA AGTATACTGC      120
CCAAGACCAC AGTGACTACA GGTATGTGGC AGCTGCTTTG GCTGTCATGA GAAATGTGAC      180
TCAGCAGATC AACGAACGCA AGCGACGTTT AGAGAATATT GACAAGATTG CTCAGTGGCA      240
GGCTTCTGTC CTAGACTGGG AGGGCGAGGA CATCCTAGAC AGGAGCTCGG AGCTGATCTA      300
CACTGGGGAG ATGGCCTGGA TCTACCAGCC CTACGGCCGC AACCAGCAGC GGGTCTTCTT      360
CCTGTTTGAC CACCAGATGG TCCTCTGCAA GAAGGACCTA ATCCGGAGAG ACATCCTGTA      420
CTACAAAGGC CGCATTGACA TGGATGCTCG AG                                     452

```

(2) INFORMATION FOR SEQ ID NO:418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

```

GATAACTTGA GATCAAATCA GTCATATTTG ACTCTTCTCT TTTTCACTCC TTTTATATCT      60
GATCAGTCAG CAGTTTTTTT AAACCCCTGT CGAAGCAGTT CTCAACACTT GTGCACCCAT      120
TCTTTCTCCT ACACCACTCA ATCTAGACCC TCACATGTGG CTGTCCTGCT TTCCTTCTCT      180
CCTACTTCTA AGCTATTCTG TGGAGAGATG TCAAAGTAAT CTTCAAAAA AATCTGATTG      240
CATCACTTCA CATCTCGAG                                     259

```

(2) INFORMATION FOR SEQ ID NO:419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

```

GAATTCGGCC AAAGAGGCCT AATTAGAAAT GGCTACTCCC CAGTCAATTT TCATCTTTGC      60
AATCTGCATT TTAATGATAA CAGAATTAAT TCTGGCCTCA AAAAGCTACT ATGATATCTT      120
AGGTGTGCCA AAATCGGCAT CAGAGCGCCA AATCAAGAAG GCCTTTCACA AGTTGGCCAT      180
GAAGTACCAC CCTGACAAAA ATAAGAGCCC AGATGCTGAA GCAAAATTCA GAGAGATTGC      240
AGAAGCATAT GAAACACTCT CAGATGCTAA TAGACGAAAA GAGTATGATA CACTTGGACA      300
CAGTGCTTTT ACTAGTGGTA ACGGGCTCGA G                                     331

```

(2) INFORMATION FOR SEQ ID NO:420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

GAATTCGGCC AAAGAGGCCT AAGAGCATTT ACCTGTCCTGA CAATTGTATT TTTAATGATA	60
GTTTGCTTTT ACTTGGTCTT TATATATTCA ATTACAAATT ACTGATATTT TGTTTAAATC	120
TACCACATTT TTCCATTGGA CTGTTTATTT TTATGTCCTT TCTTTCTTTT AGATTAAGTC	180
TTTTTCTTC TCACCCCTC ACCCTCCCC CCTGTTATA CATTCTTTTA CTATTCTTTT	240
TGTTATTCCA TAGTTGCAGC AACTCGAG	269

(2) INFORMATION FOR SEQ ID NO:421:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 405 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

GAATTCGGCC AAAGAGGCCT ACATTGAGGT AAGAGATATT TAAAAGGTTT TTAGGTGAAA	60
TTTGAAGCAG GGATGAGATT GGGATTCCAC CTTTGTGTCC ATGCATACCT GTTGATAATC	120
AGCTGTTTCT GTATCGACTC CGTGTCAACT CCAGAGCAGG GGGTATCCTC CTGTAGTGCA	180
CCTTCTCTCT TGGCCTGGAG GCAGCACTTT CTGTGCCTGG GCAGCAGAAA TGGGGAATGT	240
TCTTTGGTCC GTTGGAAAA CCGGCCCAA CATCTAGCCC TGTGCATAA GGCATGGAAT	300
TGCCCAGTTG GGGAGGACCT GTGCTGGAAA GGGATCATCA AACTCCATCT GCCCATCAG	360
ATGCCTGAAC TCTTGATACA ACTCTGCCA TCCAAGCTAC TCGAG	405

(2) INFORMATION FOR SEQ ID NO:422:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 327 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

GAATTCGGCC AAAGAGGCCT ACTCGTACTT ATTTATAAAA AAAGTAACT GTAAAACAGC	60
CTCAGGCAGG TCCTTCAGGA GGTACTCCAG AAGAAAGTAC TGTTATCATA GATGACAACT	120
CCATATGTGT TATTGCACCT GAAGACCTTT CACCTGGACA AGATGCCGAG GTGGAAGACA	180
GTGATACAGA TGATCCTGAG TATCTTAGTT TTTTGTGTTT TGTTGAGACG AAATCTCACT	240
CTTGCCCCCA GGCTGGAGTG CAATGGCAG ACCTCGGCTC ACTGCAACCT CTGCCTCCCG	300
GGTCAAGCG ACTCTCCAAG CCTCGAG	327

(2) INFORMATION FOR SEQ ID NO:423:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 315 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

GAATTCGGCC	AAAGAGGCCT	AGAATAATAC	ACTAGTAAAA	AAAAATGTAT	GTCAGGCACT	60
GGGAAGGCCA	GTAGGAATAT	ACAAATGAGA	AGCCGTGGAT	TAGAGACTCA	CAGTCTACTG	120
GGTAAAAGAA	TACGAAAGCC	AATGTATTAT	ACTGTGGTAG	CTGCTTTAGT	AGATGTATGG	180
ATAGAAAAGT	AACAAGAGAA	GAGAATGACT	ATCTCTGCCT	AACAGAAAGA	TATTTTAAAA	240
GAAGGGTTTT	GGGGCTGGAT	TTTGAAGGCT	CAATAGGCTC	CTACCATATA	GAGAACTAGG	300
AAGCGAGTCC	TCGAG					315

(2) INFORMATION FOR SEQ ID NO:424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

GAATTCGGCC	AAAGAGGCCT	ACTATCCAGG	TTTACATTTT	AAGGCAGTCG	AGACCTTATT	60
CACGTGGTAT	ATAACAACCC	ACATTTCTCT	TTTATATGGA	ACAACACTTT	TCATTTGCGG	120
CTGGCCTTCT	CAC TAGCTTA	TGCTTTTTTT	TTTAAAGACC	TTTCTTAGCA	CTCGCTGAAC	180
TCCTCCCCCT	CACAATCAAT	CTCAGCAACT	CAGCAGAGTC	GCTTCAGTTC	ACAGCTCTTA	240
ATCCTTCACT	CCAGACTAAA	GCTAATCTTA	TGTCCTCAA	CAGCTACAAC	TCAGTGTAT	300
CACAGTTCCG	ACAGCAGAGA	CTCGAG				326

(2) INFORMATION FOR SEQ ID NO:425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

GAATTCGCCA	AAGAGCCTAT	AGAAATAATA	CCACGACCTG	CGCATTCAAA	GCTGTTGTAT	60
CTGGATTGTG	ACTGCGTGGA	AGGTGAGGC	GGGAAGACAG	GGGCTGTTGC	TTTTCGTTAT	120
AAACTCTGCA	TTACTTGATT	TTTGCACTAC	GTACATTTAC	TTTGATAACA	CTGGAAAGAA	180
TAAATTGGCC	ATGTAGTGTA	GCTTCCAAAA	AAAACATATTG	CTTGGGTTTC	AAGGTCAAGG	240
AAATTTTCATT	CTCATCAGTT	TCTTGGGAAA	GAGGAAGTGG	AATGATGTTG	TCAGAAAGTG	300
AAACCATGGG	TCATTTTCAG	AACTACTCAG	AGTAATAAAT	ATTTTTTGTC	AGTTTGTTC	360
TTACAAGTGA	AATGGTCCCC	TCGAG				385

(2) INFORMATION FOR SEQ ID NO:426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

GAATTCGGCC	AAAGAGGCCT	AAGAGATTTT	TATTATGATT	TTGATTTCTT	TACTACAACA	60
TTGCATGTGT	CTGGAGTATA	GCCATTACAC	TTTATGAAAA	AGGCAAAATG	GTCATTTGGG	120
GTGTTT TAGG	AAGTTTGCCA	AAAGGCTCCT	TTGTCATTAT	AATCCTTCCT	AAGCTGCCAT	180
CCACGGGTTT	AGGTCATGGA	TATGAAAAGT	GAAAGGGTTT	AGAGATGAAG	TAGTGTCCTC	240
TGAGTGCTTA	CCAACCTGTT	AATCTTTTGG	AGATGTTAAT	TTTTTCATAT	AGAGCCCCCT	300
AAAATCTTGA	TGGCTCTAGA	TCAGTCAAGC	CTAAGAGAAG	ACGTATTTAT	GGAAAAAAC	360
AAAAACAAA	AAAACCTTGC	TGGATTGCTA	GTAATATCTA	CTTCTTGGA	ATTAATACTT	420
CATATTTTTT	AAAAAATTA	TTGATGCATT	AGGACTCGAG			460

(2) INFORMATION FOR SEQ ID NO:427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

GAATTCGGCC	AAAGNGGCCT	AGGAAAAACA	TGAAATACAT	AAATGGATTA	ATTTTGCAAA	60
TTAATCTNGC	AAATTAATCT	ATAGCTCTTA	ATGTTTCTTC	CAAATTAAAG	GAAAAATGGA	120
TAAGGAAGTA	CTTTCTTGGC	AACTGTAGA	TGAATACTGA	ATAAAAGTCA	TTCTTTCCTA	180
AAGAAGAAAA	GTGCATTTTA	GTTTTTTAGA	AAAAATGTAA	TTT TAGAAAG	TCTCTTCTAT	240
GCAGATTTTA	GAAAGTCTTT	TCTATTTTGA	GAAAGTCTTC	TTGTATGCAG	ATTTTGTTCA	300
ACTTCCCCAT	CTGTACTTAC	CAAAGGAAAA	ATAAACAGTT	TATAGAATAT	TAATAGAATA	360
ATTATGTGCN	ATGTAAAATA	TGTTGAATCT	CCCTAATTTA	TATTTACTAT	GTGAATATAA	420
ACTACAGAAT	AAAGAACTG	TTCCTCCTTT	TATCCATTAT	TTTGTTGAAA	ACAACATAAG	480
AAATCTTACA	GATTAATGTT	CATATTAAAA	GGACTCCTCG	AG		522

(2) INFORMATION FOR SEQ ID NO:428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

GAATTCGGCC	AAAGAGGCCT	AGGTAGTTAT	CAAGAGATTT	TAAAACTTCA	ACCCTTTTTT	60
TCTTATAGTT	AGTGAAGAGA	G TAGAATATC	TCCAGTTTTG	GCTGACATCT	CTACAACCTG	120
AACAATTGGC	TTAAACTTCA	CTTGGGATTC	CCGTTTGCTT	GTTT TAGCAT	GGCNAAATTT	180
GGCGTT CACA	GAATCCTTCT	TCTGGCTATT	TCTCTGACAA	AGTGTCTGGA	GAGTACAAAA	240
CTGCTGGCAG	ACCTTAAAAA	ATGTGGTGAC	TTGGAATGTG	AAGCTTTAAT	AAACAGAGTC	300
TCAGCCATGA	GAGATTATAG	AGGACCTGAC	TGCCGATACC	TGAACTTCAC	TAAGGGAGAA	360
GAGATATCTG	TTTATGTTAA	ACTTGCAGGA	GAAAGGGAAG	ATTTGTGGGC	AGGAAGTAAA	420
GGAAAGGAGT	TTGGATATTT	TCCCAGAGAT	GCAGTCCAGA	TTGAAGAGGT	GTTTCATATCT	480
GAGGAAATTC	AGATGTCAAC	GAAAGAATCT	GACTTTCTTT	GTCTTCTTGG	AGTAAGTTAC	540
ACATTTGACA	ATGAAGATAG	TGAATTAAAC	GGTGAACCTG	AG		582

(2) INFORMATION FOR SEQ ID NO:429:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

```

GAATTCGGCC AAAGAGGCCT ACTGATCAAG TGACCCATTA CTGCGGGAAA AAACCACACA      60
TACAAAAGCC TTGACCCCA GTAATTTGT ATTGGTATAT TTACCCTGAT CTTAAACTGC      120
AAGGAATGTC CGCAATTAGA GTTTTCTTT GTTTTCTAAG TCTGAACTT GATAATCCAT      180
TTCTGCCTTC CCATGACGAG TGGACATTCC TCCAGCCAGT GGTGAGTTCC TCTTTCCTTC      240
GCTCTCAGCA AGAGCATGGG TTGCCCTCCC ATCTCGTAAG CAGAGCCTAC CACAAACGCA      300
GCTCAAATCT CGAG                                     314

```

## (2) INFORMATION FOR SEQ ID NO:430:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 556 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

```

GAATTCGGCC AAAGAGGCCT ATTGGGTCCT ATTTACAAC TTAAGAATGG AGGCATACTT      60
CAGGAAAGAA AGCACCAGTG CAGTTCCAAT TTATTATTGT ATCTGCTGTC TTGAGAGTAC      120
AGGGTGTATG AGAGTGCACA GTGGTTTAGA ATCACTATGG AATT'TAAAAA GACCCAGAGA      180
CATTAAACAAG AATCCACATT CTAAGTCGTC AGAATCCACA TTTCTGACCT TGTCTGCTGG      240
GGCCTGCTCT GTTTTGTATG GCTCAAAATA TAATCTTTT ATTGAAATAC ATGTTCTCTCA      300
TCCTGTTTCA GGGCTTCTGC CTGGAATGTT CCTCCCCCTA GCATTTGTAG GGCTGGCTCC      360
TTCCTGTCTAT GCAGGTCTCA GCTCAGATGA CCCCATCTCA GAGAGGGCTT CCCTGACCAA      420
CCAATCTACA GCCCTTCCTA GTCACTTTTT TCCACATCAC CCTCTTTATG CATGGAGGCA      480
GATAGGTGTT TTACCCTGTT TATTATTAT TATTATTTT TTGAGACAAA GTCTTGCTCT      540
GGCACCCAGG CTCGAG                                     556

```

## (2) INFORMATION FOR SEQ ID NO:431:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

```

GAATTCGGCC AAAGAGGCCT AGAAGTAACG GAAGCTACCT TGTATAAAGA CCTCAACACT      60
GCTGACCATG ATCAGCGCAG CCTGGAGCAT CTCCTCATC GGGACTAAAA TTGGGCTGTT      120
CCTTCAAGTA GCACCTCTAT CAGTTATGGC TAAATCCTGT CCATCTGTGT GTCGCTGCGA      180
TGCGGGTTTC ATTTACTGTA ATGATCGCTT TCTGACATCC ATTCCAACAG GAATACCAGA      240
GGATGCTACA ACTCTCTACC TTCAGAACAA CCAAATAAAT AATGCTGGGA TTCCTTCAGA      300
TTTGAAAAAC TTGCTGAAAG TAGAAAGAAT ATACCTATAC CACAACAGTT TAGATGAATT      360
TCCTACCAAC CTCCCAAAGT ATGTAAAAGA GTTACATTG CAAGAAAATA ACATAAGGCT      420

```

CGAG

424

## (2) INFORMATION FOR SEQ ID NO:432:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

```

GAATTCGGCC TAAGNGGCCT ACATAAAAGT AAGAAAATAT CTTACTAAAA TCTCTTTTCT      60
TATAACATTT AGNTTACGTA TATATTTTAT CTCCCTTTTT TTGNAATATA TATAAATCAA      120
ATAACAGCTG AATAAACCTT TGGTCTTTTT TTTTTTTTTT TGTCTCAGGA TTGTCTTTAT      180
CTGGGACCCG AGATTAATTG CTTCGTTTTT GCTTTGGCAA AAGATTGTTT TTACAATTTT      240
TAGTCTTTTA AAGTTGACAC AGATTGTGTC AGTCTTGCTC ATTCTAAAAG CACACAAAAG      300
TTGAGCATAA AAATAGGATT AAATTTAGCA ATAAAGAATT ATAAAGACTA AAAGATACTG      360
AGTAAGTTGT TTGACAGAAA CCTGATTATC CATGATGATT ATTTGCAGGC TTCTCGAG      418

```

## (2) INFORMATION FOR SEQ ID NO:433:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

```

GAATTCGGCC AAAGAGGCCT AGAACTCCAG AGGCAAGTGT TATATGAATT ATGCATTGTA      60
TTCTACATGT TTATTAGACA TGTATGCGAG ATACATTAT ATTTTACTAA TGGTTATGAT      120
GACTTTAATA ACTTCAAAG GATTATGGGG ACTCGAG                                157

```

## (2) INFORMATION FOR SEQ ID NO:434:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

```

GAATTCGGCC AAAGAGGCCT ATGTTTTTAC TACTATTATT TTTTTTTACC CAAGGGAGAA      60
AGACAAAAAA ACGGTGGGAT TTATTTAACA TGATCTTGGC AAACGTCCTC TGCCTCTTCT      120
TCTTTCTAGA CGAGACCCTC CGCTCTTTGG CCAGCCCTTC CTCCCTGCAG GGCCCCGAGC      180
TCCACGGCTG GCGCCCCCA GTGGAAGTGT TCCGGGCCAA TGAGCTGTGT GCCGCCGAAT      240
CCAACTGCAG CTCTCGCTAC CGCACTCTGC GGCAGTGCCT GGCAGGCCGC GACCGCAACA      300
CCATGCTGGC CAACAAGGAG TGCCAGGCGG CCTTGGAGGT CTTGCAGGAG AGCCCGCTGT      360
ACGACTGCCG CTGCAAGCGG GGCATGAAGA AGGAGCTGCA GTGTCTGCAG ATCTACTGGA      420
GCATCCACCT GGGTCTCGAG                                440

```

## (2) INFORMATION FOR SEQ ID NO:435:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

```

GAATTCGGCC AAAGAGGCAT AAACATAGAG AAATTGGTGA TGTTAAACCT TCTGAATTTT    60
GTTTAAAGTG CACTGGGAAG TGATGGAAGG GTTTGTAGCA TAGCAGTAAT CTGATCTGAT    120
CTGATCCGGT GTGAATGTCT TTTTAGCAGA TGATTTTCATT TTACCAGCTC TCTNGAAAGT    180
TTAATCAATG TGATAGCCAT GACAGTTTAT TAAACTACTT ATTTGAGAAA GTAACGCTCCT    240
GTGGGAATCC AGATTATTTG TTTACTTCAT TTTAGATGTT AGTGCTAGCA CCCTTGTTTA    300
ATATTTGTTT TAACACTTAT ATACTTAAAA GCAGGAAATC TCGAG                      345

```

## (2) INFORMATION FOR SEQ ID NO:436:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

```

GAATTCGGCC AAAGAGGCCT AAGAACTCAC AATAAAGTAT CATATTCCTC TCTTTTGACC    60
TAGAATTCAT AGCCCTAGTA ATCTCGTTTT GATTAGATGC TTTGATTGGC AGTTATACAT    120
CTTTGATAAC ATTTTCAATG TGAAATGAAT TATCTTTTCG TTAAAGCCAT TTAAAGCAGA    180
ATGTCTATAA ATGAGGGCCC ACGAGAAGGA ATAACAAAGC AGGGGTGTTG GGGATGGTGG    240
CTGGGGAGCT TTGGTGTATT TATTAACCTG TGGTTGAGTT TTGCGATGTG TGCAAGTACA    300
CACAGCCCCG AACAACTCGA G                                     321

```

## (2) INFORMATION FOR SEQ ID NO:437:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

```

GAATTCGGCC AAAGAGGCCT AGTTTAAAAA CGTATTGTTT AATTTTCNAA CATTTAGGGA    60
TTTCCAGAT ATCTTNGTTG TNGGTTTCTA ATTTGATTCC ATTATGGTTA GAGACCATAC    120
TTGGTATGAT GAATTAAAAA AAAAAATNTA GAGGTTTGTA TATGGCCTGA AACATTTTTT    180
AGGTGAGTGT TCAGTTTGTA ATAGGAAAGA TGTGTCCTGC TGCCGTTAGG TAAAGTGTTT    240
CATAAGTAAT AATTAGGTCA AGTTGGTTGA TCGTGNTAAG GTCTGCTCTA TCCTTGCTGA    300
TTTCTGTCT GCTTGTTCTA GTGATTACTG AGAAAGGAGT GTTGAAGTCN ACAACGATTG    360
TTATGGGTTT GTTCTCTTTC TCCNTGAAAT TCTGTCTGNN TATGCGTCCT GTATTTTGAG    420
GACCCCTCGA G                                     431

```

## (2) INFORMATION FOR SEQ ID NO:438:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

```

GAATTCGGGC TTCATGGCAT ANGAGAGGT TCCGGGNCCA GNNCANGCNC GGGACAAGNT      60
CAGAGATGAN GTTCCCCANA GTNATGNNGA ACTCCAGTNC CCGNTGTCCC CGGNTTTTCT      120
CTCTTGTGGN ACATGGGGAN NTNTGGANTC CAGCTCCCAG NACTGGAGTG CTATTCAANT      180
GATCNAGGAN GGAAGTGACA NAAATGTTT TNTTTTNTT TNTTAAAAAA GNAGNNNCNN      240
GGGATCNGA AGNAGATGAA TGCCCTCAAA GGCCATGNAT GTACTTCAAA NGAAGTGGNT      300
NNTGAAAACA GNTNNAANAA TGTAANCGA NAGTNAAAAT NNATGTTGNG GANGAAGGAA      360
NTTGGTGGNN AGTNAAAAAA GAAGTAANCC GA                                     392

```

## (2) INFORMATION FOR SEQ ID NO:439:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

```

GAATTCGGCC TTCATGGCCT AGGTGTGCTT CCCTTTCCCC ATTTCCCATT ATTCCCAGCT      60
GTATAGTAGT GTAGTGAAAA TCACTTGAGA TGTGGAAGAG TAGTCTGGTC TAGGAAGAGA      120
GAGGGAAGAG TAAGTTTCCC AGGATAAGAG GGGGAAAAAA GGCCCCAAAG CTTTCTCAAT      180
GAGGAATGGG GAAGGAGGTT TTGCTGCCAG GTTTTACTAA GTGCATTGTA ATGAACCCTC      240
CTATTGTAGT CCTCTTTTAT TAATGCTTTC CTGACATTTA CCCTGTTAGT TGAGGCTACT      300
CGAG                                     304

```

## (2) INFORMATION FOR SEQ ID NO:440:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

```

GAATTCGGCC TTCATGGCCT AATCACNGNA GTGACTGACA TTATATATTA NGGATCAAAT      60
TATGTCCACA AGCAATATTA TATAATCTAC GTAGAAGTCT AATAACAAAC AAGAGTACAC      120
TTAAATTTAC TTTAAAGAT GTCTTTAGTT CATTCCAATA TAATCTTGA TTAATTTAG      180
GATTATTTCT ACATTTTAGG ANNTACAAAG GATCACGGGT AACATGGATT GGGNCCANAT      240
ATTTTTTTAA AGTTTCGAAT TGGTATCTGT AGTAGTGGAA TGTATAGAT TTGAAGTAAC      300
TCTCCACGGA CAGTGCTGCT TTCGTGTAGA GCAATTTAAT TGGAGAAGTG GCCATTCTTA      360
CTTCAGGGAT GCAAAGATGG TCTCATACCA TTTGGATAAA TGTCGTGGTA TCCATGCTTT      420
TTTTCAACTA ATAACATCAT CTCTCTTCAT GACCAGTTAA TTGGGCTATT TGGCAGCCCA      480

```



GTGAACCTAT GTACTAATGG CAAGTTAGGG GCAAATGGAA ATGGACACAT CCGATAAAGT 540  
 TGAAATGTAT GTTTAAATCT TTCACAGAAG TCCCTCGAG 579

## (2) INFORMATION FOR SEQ ID NO:441:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 556 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

GAATTCGGCC TTTATGGCCT ACCTACGGTA CCTGAAAACA ACGATGGCAT GGAAACACC 60  
 TCCCATTTAC CTGTTGTTGC TGCTGTCTGT TTTCGTGATT CACCAAGTTT CNTCTCAAGA 120  
 TTTATCNCC TGTGCAGGGA GATGTGGGA AGGGTATTCT ANAGATGCCA CCTGCAACTG 180  
 TGATTATAAC TGTCAACACT ACATGGAGTG CTGCCCTGAT TTCAAGAGAG TCTGCACTGC 240  
 GGAGCTTTC TGTAAAGGCC GCTGCTTTGA GTCCTTCGAG AGAGGGAGGG AGTGTGACTG 300  
 CGACGCCCAA TGTAAAGAGT ATGACAAAGTG CTGTCCCGAT TATGAGAGTT TCTGTGCAGA 360  
 AGTAAAGAT AACAAAGAAGA ACAGAACTAA AAAGATACCT ACCCCCAAAC CACCAGTTGT 420  
 AGATGAAGCT GGAAGTGGAT TGGACAATGG TGACTTCAAG GTCACAACCT CTGACACGTC 480  
 TACCACCCAA CACAATAAAG TCAGCACATC TCCCAAGATC ACNACAGCAA AACCAATAAA 540  
 TCCAGGACC CTCGAG 556

## (2) INFORMATION FOR SEQ ID NO:442:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

GAATTCGGCC TTCATGGCCT ATTATTTTGG CACCAGCGTC AAGACAAATA ATATCCTCTC 60  
 CCATTATTTT CATAAGTAAC ACAGATTCCT TGATTTTTAA AACTAAAAA TACAGCTAAA 120  
 CCTTCTTAT GTATAAAGTA TGCCTATCAT ATACAGGGAG AGGTGGGTAA TAACTTCCT 180  
 GTAATGACAG TGTGTTGGCAT TTCTTTATGG ATGGAATTGG AACATGAACA AGACCATGTC 240  
 CAGCGTTTTT ACTGTGAATG TAAATGGAAC AGCAGCCCAA AGCTGTTGTC TGTGCCCCAG 300  
 AGGTGCTACC TGTAGACAGG GACCAACTCC ATGTGTGTGT GTTAAGTGTT TGAATCCAAT 360  
 TAAGACTCCC AAGCAAATCC TGCATATTCC AAATGTAAAG AGTACTCAGT GGGAAAAAGG 420  
 TTGTTACCTC AAAGTCATTG CTTCTTTCCT GGCTGGGTCA CAGGGTGAAG AGATGAAGGT 480  
 GTCTGATGTA TATAGACAAT TAGGGAAAAA TGAGCGGCTT TCCTCGAG 528

## (2) INFORMATION FOR SEQ ID NO:443:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

GAATTCGGCC	TTCATGGCCT	ACTGGAATCT	GCAGCCCCCA	CATGCATCTG	TCTAACGCAT	60
GCCTCGTGTT	CGTTTTGCAA	ACATGCCTGT	GGTGGAGGGT	GGTCAGTTGT	AGCCCTGTGC	120
GTCTCAAGGC	TGCCTTGTA	GGCCATTCCC	AGTGCCTGCC	CTTGAGCTCC	TTACCACCCC	180
TTTTCTGCT	CGGCCCTTTA	ATCCCTGACA	GACCTGGACT	GTGTGGCTGA	AGGGGGACCT	240
GCAGCACTGC	AGAAATGCCT	CTGCGTGGTG	CCATGAAGGA	AAGAAACCTT	GGCCTGGTCT	300
CGAG						304

## (2) INFORMATION FOR SEQ ID NO:444:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

GAATTCGGCC	TTCATGGCCT	AGGGCAGGGG	GAGGGGTGCA	NAGTGGGACC	CTCACCACAG	60
GGTACTGAGA	CAGGTCATTG	TAGGTCCGCC	CCGCAATGGT	GTTGAGTTGC	ATCAAGTACT	120
CGAAGTTGGA	TATCTCAGC	TGTACCCATT	TCTGGGTAAG	GCCTGAGGCA	CGCACCATCT	180
CCTGGGGGGA	GCGGCTGCTT	AGGTAGCCAA	GAGAGGGGGG	CCGTAGGCGC	AGGANCCACG	240
AGTACACCTG	GCCCCATCCC	ACCCCATCCC	TCGAG			275

## (2) INFORMATION FOR SEQ ID NO:445:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

GAATTCGGCC	TTCATGGCCT	AACCAGCTTT	AATTTCAATT	GAGGAATAAT	AACAACCCTA	60
GAGATTGATA	GGAAAGAGCA	TGAAATACA	TTTTTTGCAT	AAAGATACCT	AAAACCATCT	120
ACCCAGCTTA	GGGTGAACT	GAATTTCTGT	GAAATAAATT	TGTTTTAAAT	ACTAATTATT	180
TTAAAACTAC	TTAATTCCTA	AAAACAATGT	CATCAGTTTC	AAAAGTTTCA	CTTTGGGAGG	240
ATATTCCTTA	AAAGGCATAC	ATAGATGGTA	AAGTATAAAA	TATTTCTGAC	AGAATTATTC	300
AGTATTATTC	AACATTTACT	TTCATGTTTG	TTATTGTACC	ACAAAGATAG	TGTCATTGTT	360
GGTTAAAAAT	GTTGGCTGTT	TTGTTAATA	TACTTAAAC	TGTAACCACT	GGCTCGAG	418

## (2) INFORMATION FOR SEQ ID NO:446:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

GAATTCGGCC	TTCATGGCCT	ACTACATCAA	GCACCAGAAC	CGCCAGCTGC	GCGCCCTGTT	60
GCTCAGCCAC	CAGTTCAAGC	GCCGGGAGGC	CGACCAGACC	CACGCACAGA	ACTTCTCCTC	120

CGCCGTGAAG	TCCCCGGTCC	AGGTCATCCT	GCTCCGTGCC	CTCGCCTTCC	TGGCNTGCGC	180
CTTCCTACTG	ACCACCGCGC	TGTATGGGGC	CAGCGGACAC	TTCGCCCCAG	GCACCACTGT	240
GCCCCTGGCC	CTGCCACCTG	GTGGCAATGG	CTCAGCCACA	CCTGACAAATG	GCACCAGGCT	300
CGAG						304

## (2) INFORMATION FOR SEQ ID NO:447:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

GAATTCGGCC	TTCATGGCCT	ACAGAGATGG	ATTATCCTAC	TTTACTTTTG	GCTCTTCTTC	60
ATGTATACAG	AGCTCTATGT	GAAGAGGTGC	TTTGGCATAC	ATCAGTTCCC	TTTGCCGAGA	120
ACATGTCTCT	AGAATGTGTG	TATCCATCAA	TGGGCATCTT	AACACAGGTG	GAGTGGTTCA	180
AGATCGGGAC	CCAGCAGGAT	TCCATAGCCA	TTTTCAGCCC	TACTCATGGC	ATGGTCATAA	240
GGAAGCCCTA	TGCTGAGAGG	GTTTACTTTT	TGAATTCAAC	GATGGCTTCC	AATAACATGA	300
CTCTTTTCTT	TCGGAATGCC	TCTGAAGATG	ATGTTGGCTA	CTATTCCTGC	TCTCTTTACA	360
CTTACCCATG	GGAAGTCGAG					380

## (2) INFORMATION FOR SEQ ID NO:448:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

GAATTCGGCC	AAAGAGGCCT	AAACAAATGA	GGGTAGTAAT	TTTTTATCTG	CTAAAACTTA	60
TATTTATATC	ACATACTTGT	TGCAATGATT	TCAGTGTCTA	CATAAATGGT	GGCTTAGCTG	120
AGGCAGGTCT	AGAATTCAAT	CGAG				144

## (2) INFORMATION FOR SEQ ID NO:449:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

GAATTCGGCC	AAAGAGGCCT	ACTAGACGTT	TGTACAAACT	ATTCCCTTGA	GTTATTTTCT	60
CTGGCTCTTC	AGCTCCTTCC	TCCCACCCCC	TCCCCTGCAC	CACCAATCCA	TTCTTTTGCT	120
TAATTTCTCT	CCATCCTTCA	GGTTTCAGCT	TTAAGAGGTC	ACTTCTTTTA	GGAGACATTC	180
CCTGAATCCT	CTCACCTCCA	CCCACAAAAA	AGGCCTCTCC	AGATGCCCTT	CTTTTCTGCT	240
CAAACCTCAT	CTGCTTCCTT	TATCATATGC	TTATCGTTTT	GGATTGTAAT	TATTTATTTA	300
ATTGCATGTC	TTTCTGCTAG	TTTTTGTTGT	AGCAACAACA	AGGATCTCGA	G	351

## (2) INFORMATION FOR SEQ ID NO:450:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

```

GAATTCGGCC AAAGAGGCCT AGATGATGGC AGGAATGAAA ATCCAGCTTG TATGCATGCT      60
ACTCCTGGCT TTCAGCTCCT GGAGTCTGTG CTCAGATTCA GAAGAGGAAA TGAAAGCATT      120
AGAAGCAGAT TTCTTGACCA ATATGCATAC ATCAAAGATT AGTAAAGCAC ATGTTCCCTC      180
TTGGAAGATG ACTCTGCTAA ATGTTTGCGT TCTTGTAAT AATTTGAACA GCCCAGCTGA      240
GGAACAGGA GAAGTTCATG AAGAGGAGCT TGTTGCAAGA AGGAAACTTC CTACTGCTTT      300
AGATGGCTTT AGCTTGGAAG CAATGTTGAC AATATACCAG CTCCACAAAA TCTGTCACAG      360
CAGGGCTTTT CAACACTGGG AGTTAATCCA GGAAGATATT CTTGATACTG GAAATGACAA      420
AAATGGAAAG GAAGAAGTCA TAAAGACAAA AATTCCTTAT ATTCTGAAAC GGCAGCTGTA      480
TGAGAATAAA CCCAGAAGTC TCGAG                                     505

```

## (2) INFORMATION FOR SEQ ID NO:451:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

```

GAATTCGGCC AAAGAGGCCT AGTCGTAAGT TACCATAATA GGTGCTTGCA GTCATTGATA      60
TAATCCAGAA AGCTAACGAA ATGCAAATGA TCAGGCTCAG TATAACTATA TTAGTTATCA      120
TCTTTATATA TCTTTTGCAT ATATTGTCGT TAAGATCTGT CATGGAAAAT AAGGATATGA      180
GCTCCTGCGG GAAAGAATAT TTAGCGTTTC GGAGAGAAAG TCATTTACGA TGTGAGCAAG      240
ACACTTGTTT AGAGGCAAAC ATAAATCCCA ACATATTCCA CCGACCAAAC AAGCATAAAA      300
ATCACAACAAA TTCAACTCC TTCCGGAAAC TCCTACTGGC CCTCGAG                                     347

```

## (2) INFORMATION FOR SEQ ID NO:452:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

```

GAATTCGGCC AAAGAGGCCT ATCTTACTAT TTTTATGTCA TTGGTTTTTT CTTCCTTCTT      60
TCTTTCTTTT TTTTCTTTT TTTTGTAGGC AGAGTCTCGC TCTGTGGGGA CACTGTTCCG      120
TTCAGAGGCC CCTCCCAGCC ATGGGGTGGG GGACAGTGGT GGGCGTGGGA ATCCCAGCGA      180
GCATCCTGGA GGGTGCGTCG TCTCCATGTA TTTTGCTCTT CCCCATCTTT TCCATGGGGT      240
CCCCTGCCAG GGTCAAGCAC TAATATGTGG TGAAGGCAGC AAACAGCGTC GGCCTCCCTT      300
TAGGGGTGGG GAGAGGGCTG TAGCACCAAG AACCCTCTCC CCCGCCACG ACATCCCTGA      360

```

AAAGGAGACT AAAATAAAGC CCCGGCGCCT CGAG

394

## (2) INFORMATION FOR SEQ ID NO:453:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

GAATTCGGCC AAAGAGGCCT AGGAAAAACA GAGTAAAAAA TTGCAAAAGA AGAAGGAAAC	60
AATAACAGAG TCAGCTGGTC GACAACAGAA AAAGAAAATA GAGAGACAAG AAGAGAAACT	120
GAAGAATAAC AACAGAGAT TATCAATGGT TCGAATGAAA TCCATGTTTG CTATTGGCTT	180
TTGTTTTACT GCCCTAATGG GAATGTTCAA TTCCATATTT GATGGTAGAG TGGTGGCAAA	240
GCTTCCTTTT ACCCTCTTT CTTACATCCA AGGACTGTCT CATCGAAATC TGCTGGGAGA	300
TGACACCACA GACTGTTCCC TCGAG	325

## (2) INFORMATION FOR SEQ ID NO:454:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

GAATTCGGCC AAAGAGGCCN AGGGTCACAG GGTGTTATC TCACTTCGCA GCTTTTCCTT	60
TCTGAGGCCA GAAAAGGAAG GGGTTTGCTT TCCTCTAGTA TTTATTCTTC TGGACTACAT	120
CAAGTACTCT AAGCCTGATG TTAGGCAATA ACTGCCCAT T AGCCATTGGC TACATTGGCC	180
TCTTTCTTGT TCCAACAATA TTAGTGATCT GTGGNACAGG ACACACTCTT TGTTTGCTAG	240
CTACAAATTC TAACAAAGCT AAGTTTATT CATGTAGNTA TTCACAAATT AANACACAC	300
ACACACCACA CACACACACA CACACACACA CACACACATA CCACAAAACC	360
CAGAGATCAC CAAATACTAT ATAAATAAAC AAGCCCAAAG TCACAGATCA GGGACACTCG	420
AG	422

## (2) INFORMATION FOR SEQ ID NO:455:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

GAATTCGGCC AAAGAGGCCT AGACGTCCAA GAAAAACAT TTGGTGAAAG TCAGGATTTA	60
CCTTTGAAAT CCGACTTGGG CACCAGGGAA GATAGTAGTG TTGCATCTAG TGATAGGAGT	120
AGTGTGGAGC GAGAAGTGGC AGAACACCTA GCAAAAGGCT TCTGGAGTGA CATTGGCAGC	180
ACGGACACTC CTTGCCAAT GCAGTTATCA CCTGCTGTGG CCAAAGATGG CTCAGAACAG	240
ATCTCACAGA AACGGTCTGA GTGTCCGTGG TTAGTNTCA GGATTAGTGA GAGCCAGAA	300

CCAGGTCTCA CTCGAG

316

## (2) INFORMATION FOR SEQ ID NO:456:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

```

GAATTCGGCC AAAGAGGCCT AGTCAGTCTG AGTTAGAAAA TCGACTCCAT CATCTAACAG      60
AGACTCTCAT CCAGAAACAG ACCATGCTGG AGAGTCTCAG CACAGAAAAG AACTCCCTGG      120
TCTTTCAACT GGAGCGCCTC GAACAGCAGA TGAAGTCCGC CTCTGGAAGT AGTAGTAATG      180
GGTCTTCGAT TAATATGTCT GGAATTGACA ATGGTGAAGG CACTCGTCTG CGAAATGTTC      240
CTGTTCTTTT TAATGACACA GAAACTAATC TGGCAGGAAT GTACGGAAAA GTTCGCAAAG      300
CTGCTAGTTC AATTGATCAG TTTAGTATTC GCCTGGGAAT TTTTCTCCGA AGATACCCCA      360
TAGCGCGAGT TTTTGTAATT ATATATATGG CTTTGCTTCA CCTCTGGGTC ATGATTGTTC      420
TGTTGACTTA CACACCAGAA ATGCACCACG GCCTCGAG      458

```

## (2) INFORMATION FOR SEQ ID NO:457:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

```

GAATTCGGCC AAAGAGGCCT ATCGAGGTTT GGTGACTGA TGAAGCTTT TATTTCTTTA      60
ACCATTTATG CATTCTCTCA ATTTGCTACA ATAAACATAG ATTGCACAGG GGTGAATACT      120
AAGGAAGTCG GAGGGTTAGG GTTAATTTCT GTGAAAGACC AAATATGTTT CTCTGGTTCT      180
CTCGAG      186

```

## (2) INFORMATION FOR SEQ ID NO:458:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

```

GAATTCGGCC AAAGAGGCCT AGCATTATGG TATATTTTAA ATTCATCAAG CTCATCTGTA      60
TGTGTCCTTT TGTCCTTTTA CTAAGTATGG GATTGGGGCT GGGATCATGG CAGCCTGCTC      120
TGATGTATTT CTCTCCACTC TATTTTATTA TTTTAAAGAA GAGTTCTAAC TTAAATACGT      180
GGACCAGCTA TTGGATAACT TTAATTCATA TATTTATCAT TCTTTCTATT CACTTTGCCA      240
CATACACACC ATGTGATGAT TTTAAACCCG ATTTCTGTAT AGAGAATGTT AAAAGGATAG      300
CACTCGAG      308

```

## (2) INFORMATION FOR SEQ ID NO:459:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 303 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

```
GACATGCTGT GGTTCACCG CGCACTCACC CTGCTCATCA TCCTCCGCCA CTCACCAGG      60
AAGGACCCAC AGGGGCTGGG CGTGACGAGT GACGCCATCG CCGATGCCTG CCAGGCCCTG      120
GTGGGCCCCA CCGCCACAG CCGTTGCTGG TGATCTCCGG GATCCCCACC CACCTGGACG      180
AGGGCGTAGT CAGAGGCGCC ATCCGCAAGG CCTGCAACGC CCACGGCGGG GTCTTCAAAG      240
ACGAGATCTA CATCCCGCTG CAGGAAGAAG ACACCAAGAA GCCAAAAGAC AAGGCCGAGG      300
GCG                                         303
```

## (2) INFORMATION FOR SEQ ID NO:460:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 250 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

```
GAATTCGGCC TTCATGGCCT ACACTTTAAT TGCTGTTATC ATGGGCCTAA TTACAGTCAC      60
TGCACTGGCC ACCACTGCCG GAATGGCATT ACACCACTCC ATTCAAGCGG CTCATTTTGT      120
TAATGGTTGG CAAGCCAATT CCATCCAAAT GTGGAATTCT CAACAAGGCA TCGATCGAAA      180
ATTGGCAAT CAAATTAGTG ATTTAAGACA GTCTGTTATT TGGCTTGGAG ATCAGGTAGT      240
GAGTCTCGAG                                         250
```

## (2) INFORMATION FOR SEQ ID NO:461:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 309 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

```
GGTGACGCCT GCTTCACATC TCTAATGAAC ACCCTCATGA CGTCGCTACC AGCACTAGTG      60
CAGCAACAGG GAAGGCTGCT TCTGGCTGCT AATGTGGCCA CCCTGGGGCT CCTCATGGCC      120
CGGCTCCTTA GCACCTCTCC AGCTCTTCAG GGAACACCAG CATCCCGAGG GTTCTTCGCA      180
GCTGCCATCC TCTTCCTATC ACAGTCCCAC GTGGCGCGGG CCACCCCGGG CTCAGACCAG      240
GCAGTGCTAG CCCTGTCCCC TGAGTATGAG GGCATCTGGG CCGACCTGCA GGAGCTCTGG      300
TTCCTCGAG                                         309
```

## (2) INFORMATION FOR SEQ ID NO:462:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

```
GAATTCGGCC TTCATGGCCT AATGAAGAAA AGCAGAATTC CAAATTCAAA CTGTTGGAGT    60
GAGCCAAGTG GACAGACCCT CCATGAGTGC ACTTTCTTCC AAGAAATCCC CAGATTTACC    120
CCATAGAGGT CTGGGATTAC CTGGAATATA ATATGAAAAA CATTTTTtag GCTGGGTGTG    180
GGGCTCACAC CTGTAATCCC AGCACTTTGG GAGGCTGAGG CGGGCGGATC ACCTGAGGTT    240
GGGAGCTCGA G                                     251
```

(2) INFORMATION FOR SEQ ID NO:463:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 225 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

```
GAATTCGGAA CAATGGGGGT TTCAAACAT AAAAGTGAAA GTCCTTGTA ATCTCCTTAT    60
CCAAATGAGA AAGACAAGGA AAAAAATAAG TCAAATCTT CAGGCAAAGA AAAAGGCAGT    120
GATTCATTTA AATCTGAGAA GATGATAAA ATCTCTCCG GTGGCAAAAA GGAGTCCAGG    180
CATGATAAAG AAAAGATAGA AAAGAAAGAG AAACGGGACC TCGAG                                     225
```

(2) INFORMATION FOR SEQ ID NO:464:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 527 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

```
CTCGAGGCGT GTGGGATCAT GAGGCAAAGA AAGTCCAACG AGGGAGAGAG GAGAGTGAGG    60
GATGAGAGGG GACACTTGCT CCATCCTAGT CCCCACGCGG CCCAGCTGGC TTCCTTTTCC    120
AGAATATCTC CTTGCTATAA CCTGGCAGCA GGGGAGCCAA GGTCTTCTC CATCCTTACA    180
GGCACTGAAC CAGGATGTAG GCGCACACTG CTGTGTTCTC TCTGGCCCAT CCTCTCTAAT    240
TGTCTTTCCC TTCCAGGTC ACAGGATGCT TATTCTCATC TCCAGGCCTT TGCACGGGCC    300
GGGCCTGCTG CCAATCCCCG CACTCTCCCC TTCTTAGGGC CAGGCTAACT CTTCCCCATC    360
CCCGGGGCTC AAGCGTTCAG GTCTCTTCCA AAAGCAGTCT TGGTGGTCCC TGCCACGCGT    420
TACCCTCCTC TCAAGTCACC CGGGAGGTGG AGGTTGCTGT AAGCCAAGAT CGCAGTGAGC    480
TGAGATTGCA CCATTGCACT CCAGCTAGG CCATGAAGGC CGAATTC                                     527
```

(2) INFORMATION FOR SEQ ID NO:465:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 317 base pairs
  - (B) TYPE: nucleic acid



- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

GCACTCATAA AAATCTTACT CAGAAATCTT CAGAGGTTTG CTAAGGATAC AATTTGATTC	60
TTACACATTT AATGCTCACC AGCTGCTTAG GCCCACACCA TTTATCCACC CTGATTGCT	120
ACTGCTCTTT GAAATACAAC CAGTGTTC A GCCAGACTGT TTTCTGCTT CTGCTCCCT	180
TCTCTCCTC CCAGCACATC TGTGAATTCT TTGACTGGT TACCACTCCC AAACCTCTCC	240
CCAGCAATGC AGATCTTCTA CACCTTTAG GATCTAAGCT AAGTCTGCTT CCCAGATATC	300
CTCCCGAACA GCTCGAG	317

(2) INFORMATION FOR SEQ ID NO:466:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 348 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

GGTCATTCTT TCCATCGCTG CGGACACGGG AGTCAGAAGT GAAACAGTCC TGTCTCGTG	60
GGGCTTACGT TCCAGGCGCA AGAGCCACAG GTAGTCGAAT TGGGAACCG CCTCGGATGT	120
CACATAAGCG CCCAGGGAGG ACAGGGCAGG ACAGGGCCTC CCTGGGGAGG TGAAGTGTAGT	180
CAAGACTCAA AAGAGGGAAG CGAGGGAACA AGCCATGCGA GGAAGTAACG AAGGAACATT	240
CCAGAAAGAT TTCACATCCC AAGCCTAAG TCCAGGGGCA GCAGGCATTG AGGCGGATGT	300
GGCTGGAGTG GAGAGAAAGA GGAATTAATA GGATGGCATG AGCTCGAG	348

(2) INFORMATION FOR SEQ ID NO:467:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 293 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

GAATTCGGCC TTCATGGCCT ACGAGGAAAG ATCTAATTAT CATGGACCTG CGACAGTTTC	60
TTATGTGCCT GTCCTGTGC ACAGCCTTTG CTTGAGCAA ACCCACAGAA AAGAAGGACC	120
GTGTACATCA TGAGCCTCAG CTCAGTGACA AGGTTACAA TGATGCTCAG AGTTTTGATT	180
ATGACCATGA TGCCTTCTTG GGTGCTGAAG AAGCAAAGAC CTTTGATCAG CTGACACCAG	240
AAGAGAGCAA GGAAAGGCTT GGAAAGATTG TAAGTAAAT AGGCTGGCTC GAG	293

(2) INFORMATION FOR SEQ ID NO:468:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 279 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

```
GAATTCGGCC TTCATGGCCT AATAAATTGC CAGCATANTA AAAAAGTGGC TTACACTCAA    60
TTGCTACACC TTTTCACAGG CAAAAGGTTT TATTCTCTCC TAAATTAATT TTATCCCGTT    120
TTTTTTTACC ACCTAACTTT TGCCTTTTAT TCAGAACTAA TGTATTTTTT TCTTATTGTC    180
GTTTTTTTTT TCAAAATTCC CTCCTCGGTG GAAAGTAAAG GAGTAGGAAC ATACTATTAT    240
TCAACCAACA TGCAGCAACC CTTACGTACG GTCCTCGAG                               279
```

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

```
GAATTCGGCC TTCATGGCCT AAGTTTTGAA AAAAAAATC TTTAAGTGGA TTGTGAGTAG    60
ATTTTTTTAA GGAGCATTTT TATAATATTT TTCCTGAATC CTTGCATATT TGACAGTGTG    120
TTTCTATTGT GTTTATGTGT GGCAGCAATT TACTTTATAT CAAAGTTTTT TGTTTTTGTT    180
TTTGTTTTGT GAGACACAGT CTCACCTAT CACCCAGGCT GGAGTGCAT GGCATATCT    240
CGGCTTACTG CAGCCTTGAC CTCCAGACT CAAGTGATCC TCCCACCTGC CTCGAG        296
```

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

```
GAATTCGGCC TNCATGGCCT ATGTTTTTTA TATATGGATT TATTTTTGCT TTTTAGGCT    60
GATTCAGTGT GAAAATGAGG TAGGGAAATT GTTGTTTATC ACAGAAATCC CAGAATTAAT    120
ACTGGAAGAC CCCAGTGAAG CCAAAGAGAA CCTATTCTG CAAGAAACAT CTGTGATAGA    180
GTCGCTGGCT GCAGATGGGA GCCCAGGGCT AAAATCAGTG CTATCTACAA GCCGAAATTT    240
AAGCAACAAC TGTGACACAG GAGAGAAGCC AGTGGTTACC TTCAAAGAAA ACATTAAGAC    300
ACGAGAAGTG AACAGAGACC AAGGAAGAAG TTTTCCTCCC AAAGAGGTGA GAAGGGACTA    360
TAGCAAAGGA CTCGAG                               376
```

(2) INFORMATION FOR SEQ ID NO:471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

GAATTCGGCC	TTCATGGCCT	ACAAGATTGG	CAAGATGCTT	ATTTTGGTG	CCATATTGG	60
CTGCCTTGAC	CCAGTGGCAA	CACTAGCTGC	AGTTATGACA	GAGAAGTCTC	CTTTTACCAC	120
ACCAATTGGT	CGAAAAGATG	AAGCAGATCT	TGCAAAATCA	GCTTTGGCCA	TGGCGGATTC	180
AGACCACCTG	ACGATCTACA	ATGCATATCT	AGGATGGAAG	AAAGCACGAC	AAGAAGGAGG	240
TTATCGTTCT	GAAATCACAT	ACTGCCGGAG	GCTACTCGAG			280

## (2) INFORMATION FOR SEQ ID NO:472:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

GAATTCGGCC	TTCATGGCCT	AGCAGTAAGC	CAGGATTGCA	CCACTGCACT	CCAGCCTGAG	60
TGACAGAGTG	AGACTCTGTT	TCAAAACAAA	ACAAAAAACT	TTACAGCAAT	CCTGGTCCCT	120
ACCATGGAGC	ATGTGTTACA	GGAAAACAGC	CAGTCCACTC	TGCAACCAAT	TTGGACATGG	180
CCCTGAAAAT	CCTTTTGTGA	CAGAAAGGGG	AAAATAAGAG	TACTGGCAGA	AAGTCAGATG	240
CTGGGGATGC	CTCACCCTCT	AGTCTCATGA	CTATCACACA	TGAGACGGTG	TTCCGCTGTA	300
ACTTTTCCCC	CCCCCCCCC	CGTTTGTGGA	TCTGAATCTG	GAAAAGAGCT	TGGAGAGATT	360
TACAGGCCTC	CTCTTCTGCA	ATCAGTAAGA	GTACCATGTG	GAGGCAGAGA	GCCAGAATAG	420
GTTGTGGGGC	TTCTCGAG					438

## (2) INFORMATION FOR SEQ ID NO:473:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

GAATTCGGCC	TTCATGGCCT	AGAACAGCTC	TCCAATTAC	ACTTATCTGT	ACAATGTACA	60
TTAATAACTA	ATTGTTAGA	TGATTAATAC	CAATAATTAA	CTTGCTAGAG	GACCCAGGAA	120
ACAGAATATC	TGCAAGGCCC	AGAGTAGATC	ATAAATAAAT	AGGAATGCAG	ACATAAGATG	180
TTCAGTTTGT	GAACAGTAAA	GCTATAATGA	GTTTTCTTTA	AAATCAAACA	ATTGTACAAT	240
GCATTATAGT	CTACAACCTA	TTCTGTAGTT	CAAATAAATA	AAACTTTCCC	CTGTTACAGA	300
AAGACAGCCC	TCCTCCCAGC	AACATTTCAG	ACTGGATGGA	TTGATTCTC	ACCTGACATA	360
ACTCTAAAT	CCTCACTGAA	GAAGCCAGGA	AGTCAAACCTG	AGGCTGAAGA	CCTGAAAGTA	420
CAGGGGACTA	AACCCAGAAA	GCAGTAGGCC	ATGAG			455

## (2) INFORMATION FOR SEQ ID NO:474:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

GAATTCGGCC	TTCATGGCCT	ACATGGACCT	CCTGCACAAG	AACATGAAAC	ACCTGTGGTT	60
CTTCCTCCTC	CTGGTGGCAG	CTCCCAGATG	GGTCCTGTCC	CAGGTGCAGC	TACATCAGTG	120
GGGCACAGGA	CTGTTGAAGC	CTTCGGAGAC	CCTGTCCCTC	ACCTGCGCTG	TGAATGGTGA	180
GCCCTTCAGT	GGTTATTTCT	GGACCTGGAT	CCGCCAGNCC	CCCGGGAAGG	GCCTGGAGTG	240
GATTGGGCAA	ATCAATTATG	ATGGAACCAC	CAAGCACAAC	CCCTCCCTCG	AG	292

## (2) INFORMATION FOR SEQ ID NO:475:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

GAATTCGGCC	TTCATGGCCT	AAGGGTGGGC	TTTAATGGCA	GCTGGGGTAA	AAGGAAACAA	60
AAACAGTAAT	TCTGAAGAGC	ACAGGGAACA	GGCAGCCAGG	ACCAGCCTGG	CCCATTCCAG	120
GCCAGCTGAG	CTGAAATGCT	GATTCTGTCC	AGGGGGCTGC	TGTATGTGTA	GACTGGTGGC	180
AGTCTTGGGG	ACTGAGGCCT	CTTGAGAGAG	AGGGAAGACT	GTCGGCTCAG	AAGTCCATGG	240
AGCTGTGGGC	CAGGTAGTCC	TTGCCACCGA	TGTTGCTGAC	CTGCTTGGTC	TGCATAGCCT	300
CGAG						304

## (2) INFORMATION FOR SEQ ID NO:476:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

GAATTCGGCC	TTCATGGCCT	ACCAGCTCTC	TTCTAAAAGA	GAAGTGGGTG	GGCACACTGA	60
ACTGTTTGGT	GGCCCCAACC	ACAGGAAGCT	GCAATTCTCT	GGCTTAGGGT	GATACTTTTG	120
CCCTCCTTGT	GCCCCCTCTC	GGACGCTCTG	CACCAACCCC	AGGCTACTGA	GCCACCTTCC	180
CTCCTCATGC	CTTCCCTGAG	CTTTGGTGCA	TCTCATCTGG	ACTATGGGTT	GTACTGTGAC	240
CATCCCAACA	CCTCACCTC	TGTCTACAAG	GAAATGGGAG	GTGGAGCCTC	CTGGCTGAGA	300
AATTGTTTTG	CAAATGGATC	TCGAG				325

## (2) INFORMATION FOR SEQ ID NO:477:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

GAATTCGGCC	TTCATGGCCT	AAGCTCATCA	ACGAGAAGCT	CATCAGAACC	AAGGGGCTGT	60
GGGGCCCCGT	CCATGAGCTG	GGCCGCAACC	AGCAGCGGCA	GGAGTGGGAG	TTCCCAACCAC	120

ACACCACCGA	GGCCACCTGC	AACCTGTGGT	GTGTGTATGT	GCATGAGACG	GTCTTGGGCA	180
TTCCTCGAAG	CCGTGCCAAT	ATTGCTCTGT	GGCCCCCAGT	TCGGGAGAAG	AGAGTCAGAA	240
TCTACCTGAG	CAAGGGTCCC	AATGTGAAAA	ACTGGAATGC	ATGGACCGCA	CTGGAAACTC	300
GAG						303

## (2) INFORMATION FOR SEQ ID NO:478:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

GAATTCGGCC	TTCATGGCCT	AGTTGTTT	CAG AATCCACACA	GCTCTGAATT	ACCAACGCTG	60
AATTTCCAAG	ATACTGTAAA	CACCTTGACC	AACAGTCCAG	CCATCCCATT	GGAAACATCT	120
GCATGTCAGG	ACATACCCAC	TTCTGCCAAT	GTACAAAATG	CAGAGGGTAC	CAAATGGGGA	180
GAGGAGGCAT	TGAAAATGGA	TCTTGACAAT	AACTTTATT	CAACTGAGGT	GTCAGTTTCT	240
TCCACTGAAA	ATGCTGTCAG	TTCTGACCTC	CGGGCAGGGG	ATGTACCTGT	TTTATCTTTG	300
AGTAATAGCA	GTGAGAATGC	CGCCTCTGTG	ATCAGCTCGA	G		341

## (2) INFORMATION FOR SEQ ID NO:479:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

GAATTCGGCC	TTCATGGCCT	AAGTTTTGAA	AAAAAAAATC	TTTAAGTGGA	TTGTGAGTAG	60
ATTTTTTTAA	GGAGCATTTT	TATAATATTT	TTCTGAATC	CTTGCAATTT	TGACAGTGTC	120
TTTCTATTGT	GTTTATGTGT	GGCAGCAATT	TACTTTATAT	CAAAGTTTTT	TGTTTTTTGT	180
TTTGTTTTGT	GAGACACAGT	CTCACCCTAT	CACCCAGGCT	GGAGTGCACT	GGCACTATCT	240
CGGCTTACTG	CAGCCTTGAC	CTCCAGACT	CAAGTGATCC	TCCCACCTGC	CTCGAG	296

## (2) INFORMATION FOR SEQ ID NO:480:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:

GAATTCGGCC	TTCATGGCCT	ACAGAGATGG	ATTATCCTAC	TTTACTTTTG	GCTCTTCTTC	60
ATGTATACAG	AGCTCTATGT	GAAGAGGTGC	TTTGGCATA	ATCAGTTCCC	TTTGCCGAGA	120
ACATGTCTCT	AGAATGTGTG	TATCCATCAA	TGGGCATCTT	AACACAGGTG	GAGTGGTTCA	180
AGATCGGGAC	CCAGCAGGAT	TCCATAGCCA	TTTTAGCCCC	TACTCATGGC	ATGGTCATAA	240
GGAAGCCCTA	TGCTGAGAGG	GTTTACTTTT	TGAATTCAAC	GATGGCTTCC	AATAACATGA	300

CTCTTTTCTT TCGGAATGCC TCTGAAGATG ATGTTGGCTA CTATTCCTGC TCTCTTTACA 360  
CTTACCCATG GGAACCTGAG 380

## (2) INFORMATION FOR SEQ ID NO:481:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:

GAATTCGGCC TTCATGGCCT AAGTTTGTAA AAAAAAATC TTAAAGTGA TTGTGAGTAG 60  
ATTTTTTTAA GGAGCATTTT TATAATATTT TTCCTGAATC CTTCATATT TGACAGTGTC 120  
TTTCTATTGT GTTTATGTGT GGCAGCAATT TACTTTATAT CAAAGTTTTT TGTGTTGT 180  
TTGTTTTGT GAGACACAGT CTCACCTAT CACCCAGGCT GGAGTGCAT GGCATATCT 240  
CGGCTTACTG CAGCCTTGAC CTCCAGACT CAAGTGATCC TCCACCTGC CTCGAG 296

## (2) INFORMATION FOR SEQ ID NO:482:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:

GAATTCGGCC TTCATGGCCT ACAGAGATGG ATTATCCTAC TTTACTTTTG GCTCTTCTTC 60  
ATGTATACAG AGCTCTATGT GAAGAGGTGC TTTGGCATA ATCAGTTCCC TTGCGGAGA 120  
ACATGTCTCT AGAATGTGTG TATCCATCAA TGGGCATCTT AACACAGGTG GAGTGGTTCA 180  
AGATCGGGAC CCAGCAGGAT TCCATAGCCA TTTTCAGCCC TACTCATGGC ATGGTCATAA 240  
GGAAGCCCTA TGCTGAGAGG GTTACTTTT TGAATTCAAC GATGGCTTCC AATAACATGA 300  
CTCTTTTCTT TCGGAATGCC TCTGAAGATG ATGTTGGCTA CTATTCCTGC TCTCTTTACA 360  
CTTACCCATG GGAACCTGAG 380

## (2) INFORMATION FOR SEQ ID NO:483:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:

GAATTCGGCC TTCATGGCCT AGGCTGGACA GACTTTCTAA TGAACCCAAT GGTTATGATG 60  
ATGGTTCTTC CTTTATTGAT ATTTGTGCTT CTGCCTAAAG TGGTCAACAC AAGTGATCCT 120  
GACATGAGAC GGGAAATGGA GCAGTCAATG AATATGCTGA ATTCCAACCA TGAGTTGCCT 180  
GATGTTTCTG AGTTCATGAC AAGACTCTTC TCTTCAAAAT CATCTGGCAA ATCTAGCAAC 240  
GGACAGCTCG AG 252

## (2) INFORMATION FOR SEQ ID NO:484:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

```

GAATTCGGCC TTCATGGCCT ACTACATCAA GCACCAGAAC CGCCAGCTGC GCGCCCTGTT      60
GCTCAGCCAC CAGTTCAAGC GCCGGGAGGC CGACCAGACC CACGCACAGA ACTTCTCCTC      120
CGCCGTGAAG TCCCCGGTCC AGGTCATCCT GTCCTGTGCC CTCGCCTTCC TGGCCTGCGC      180
CTTCTACTG ACCACCGCGC TGTATGGGCG CAGCGGACAC TTCGCCCCAG GCACCACTGT      240
GCCCCTGGCC CTGCCACCTG GTGGCAATGG CTCAGCCACA CCGACAATG GCACCAGGCT      300
CGAG                                     304

```

## (2) INFORMATION FOR SEQ ID NO:485:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

```

GAATTCGGCC TTCATGGCCT ACAGAGATGG ATTATCCTAC TTTACTTTTG GCTCTTCTTC      60
ATGTATACAG AGCTCTATGT GAAGAGGTGC TTTGGCATAAC ATCAGTTCCC TTGCGCGAGA      120
ACATGTCTCT AGAATGTGTG TATCCATCAA TGGGCATCTT AACACAGGTG GAGTGGTTCA      180
AGATCGGGAC CCAGCAGGAT TCCATAGCCA TTTTCAGCCC TACTCATGGC ATGGTCATAA      240
GGAAGCCCTA TGCTGAGAGG GTTACTTTT TGAATTCAAC GATGGCTTCC AATAACATGA      300
CTCTTTTCTT TCGGAATGCC TCTGAAGATG ATGTTGGCTA CTATTCCTGC TCTCTTTACA      360
CTTACCCATG GGAACCTCGAG                                     380

```

## (2) INFORMATION FOR SEQ ID NO:486:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

```

GAATTCGGCC TTCATGGCCT ACAGAGATGG ATTATCCTAC TTTACTTTTG GCTCTTCTTC      60
ATGTATACAG AGCTCTATGT GAAGAGGTGC TTTGGCATAAC ATCAGTTCCC TTGCGCGAGA      120
ACATGTCTCT AGAATGTGTG TATCCATCAA TGGGCATCTT AACACAGGTG GAGTGGTTCA      180
AGATCGGGAC CCAGCAGGAT TCCATAGCCA TTTTCAGCCC TACTCATGGC ATGGTCATAA      240
GGAAGCCCTA TGCTGAGAGG GTTACTTTT TGAATTCAAC GATGGCTTCC AATAACATGA      300
CTCTTTTCTT TCGGAATGCC TCTGAAGATG ATGTTGGCTA CTATTCCTGC TCTCTTTACA      360
CTTACCCATG GGAACCTCGAG                                     380

```

## (2) INFORMATION FOR SEQ ID NO:487:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

```

GAATTCGGCC TTCATGGCCT ACAGAGATGG ATTATCCTAC TTTACTTTTG GCTCTTCTTC      60
ATGTATACAG AGCTCTATGT GAAGAGGTGC TTTGGCATAAC ATCAGTTCCC TTGCGCGAGA      120
ACATGTCTCT AGAATGTGTG TATCCATCAA TGGGCATCTT AACACAGGTG GAGTGGTTCA      180
AGATCGGGAC CCAGCAGGAT TCCATAGCCA TTTTCAGCCC TACTCATGGC ATGGTCATAA      240
GGAAGCCCTA TGCTGAGAGG GTTTACTTTT TGAATTCAAC GATGGCTTCC AATAACATGA      300
CTCTTTTCTT TCGGAATGCC TCTGAAGATG ATGTTGGCTA CTATTCCTGC TCTCTTTACA      360
CTTACCCATG GGAACGAG

```

## (2) INFORMATION FOR SEQ ID NO:488:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

```

GAATTCGGCC TTCATGGCCT ACAGAGATGG ATTATCCTAC TTTACTTTTG GCTCTTCTTC      60
ATGTATACAG AGCTCTATGT GAAGAGGTGC TTTGGCATAAC ATCAGTTCCC TTGCGCGAGA      120
ACATGTCTCT AGAATGTGTG TATCCATCAA TGGGCATCTT AACACAGGTG GAGTGGTTCA      180
AGATCGGGAC CCAGCAGGAT TCCATAGCCA TTTTCAGCCC TACTCATGGC ATGGTCATAA      240
GGAAGCCCTA TGCTGAGAGG GTTTACTTTT TGAATTCAAC GATGGCTTCC AATAACATGA      300
CTCTTTTCTT TCGGAATGCC TCTGAAGATG ATGTTGGCTA CTATTCCTGC TCTCTTTACA      360
CTTACCCATG GGAACGAG

```

## (2) INFORMATION FOR SEQ ID NO:489:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:

```

GAATTCGGCC TTCATGGCCT AGGTTTACAG GCATACCTCA TTTTATTGCA CTTCACTTTA      60
TTGTGCTTTG CAGATAATTG TGCTTTTAC AAATTGAAGG TTAGTGGCAA CCCTGTGTTG      120
AGCAAGTTCA TTGGCAACAT TTTTCCAACA GCATGTACTC ACTTGTCTCT ATGTCACATC      180
TTGATAATTT TCATATTTCC AACTTTTTC TATCATGAT GATGATTAGT GATCTTTGTT      240
ACTGTNGTAG TTGTTTGTG GGCACCACAC TGTATGCAGN AAAGCTCGAG      290

```

## (2) INFORMATION FOR SEQ ID NO:490:



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

```

GCTACCTTAA AAAATAGATA CTCCACTAGA GGCTGTGCTT AATTCAAATC CATGTGTGTG      60
CCTGCATTAC ATGTGTGAAC ACGTGTTTCT GTCGTGTGTG TCATGCACAT CTGTGTGTTG      120
CATAGCATAA GCCAAATGAA AATCATTTGT TCATGGGATT CATATGAGGA ACAAATTTAA      180
ATTTGAATAC AGTCAGATAA CTGCCACGCA GGGCATTGTT GGAACCATCC CCGAATGCCC      240
TGATGTGATT TCCCTCAGAA AATCCTTGTT ATTAGAGGAG AAGGTCTGGG CAGGGGCAGC      300
AGCATCTCAG ACATCAAGTC AACTTTATCA TCTACTACAT CAGCACTGAA GTCCAACGGC      360
ATCCTCGAG

```

## (2) INFORMATION FOR SEQ ID NO:491:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

```

GAATTCGGCC TTCATGGCCT ATGCTTTTTT CTTTATTCTT TGTAGTTGTT TAGGAGTGGG      60
GGGCCTCGCA GAACACCTAG TCCAGCCCAC TGCCAGAGC AGGTGTGTCC CTTTCATACT      120
TCAGTCCACT TTAACACAGC CTTCCCCCAC CCCCTTCTAT GGTAGCAGTT CTCCTCGGGG      180
TCTCCATGGA CACCTGTGC CCCAAGCCGA TGGCCCCACC CAGCAGCATC AGCACAGCTG      240
CCCCCTTCT CCGCAGAGCA GGCTCTCCTT TACGGGACTC TCCTCTTCCC TCCCACCCCC      300
CCTCGAG

```

## (2) INFORMATION FOR SEQ ID NO:492:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

```

GGAATAAGAA GAGAAAGCCA AGGAAGACAA GGGCAAACAA AAGTTGAGGC NGCTTCACAC      60
ACACAGATAC GGAGAANCCA GAAGTGCCAG AGTCAGCATT CTGGAAGAAA ATCATAGCAT      120
ATCAACAGAA ACTTCTAAAC TATTTTGCTC GCAACTTTTA CAACATGAGA ATGTTAGCCT      180
TATTTGTGCG ATTTGCTATC AATTTTCTCT TGCTCTTTTA TAAGGTCTCC ACTTCTTCTG      240
TGGTTGAAGG AAAGGAGCTC CCCACGAGGC TCGAG

```

## (2) INFORMATION FOR SEQ ID NO:493:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

GCCTTGGGCC	CTCGAAAGT	CTTGGAGAAG	CAGTTTACT	TCCCTTCCTT	CACTTAGACC	60
CCATTCTTTA	GCATTTCTTC	TGAAGCTCCC	ACAAGACCCA	AGAATGGCTG	CTGCAGTGTC	120
TCCTCTTCAG	TCAGGGACCC	TGGTTGAGGT	TTGTGTATTG	TTCATTATTG	CTCTGTTTTG	180
CAGTTGTCA	AAGTTGGAAG	ACTGCCTGC	GGAGCAGTGG	AACCATGCCA	CAGTCCGCAA	240
TGCCTTAAAG	GNACTGCTCA	AAGAGATGAA	CCAGAGCACA	TTAGCCAAAG	AAACCTCGA	300
G						301

(2) INFORMATION FOR SEQ ID NO:494:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 389 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

GGAAGATGTC	TACAGAAAAG	GTAACACAAA	AGGAGGAAGC	TGGGGAAAAA	AGAGTGTGCG	60
GAGACCAGAT	CAAGGGACCG	GACAAAGAGG	AGGAACCAAC	AGCTGCTGCA	TCCCATGGCC	120
AGGGGTGGCG	TCCAGGTGGC	AGAGCAGCTA	GGAACGCAAG	GCCTGAACCT	GGGGCCAGAC	180
ACCCTGCTCT	CCCGGCCATG	GTCAACGACC	CTCCAGTACC	TGCCTTACTG	TGGGCCCAGG	240
AGGTGGGCCA	AGTCTTGGCA	GGCCGTGCCC	GCAGGCTGCT	GCTGCAGTTT	GGGGTGCTCT	300
TCTGCACCAT	CCTCCTTTTG	CTCTGGGTGT	CTGTCTTCCT	CTATGGCTCC	TTCTACTATT	360
CCTATATGCC	GACAGTCAGC	GCACTCGAG				389

(2) INFORMATION FOR SEQ ID NO:495:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 438 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

GTGGCGATTG	GTCCTGTCAT	GGTTTATTCA	GCCATGTGGT	GGATGGCTAC	TTGTCTTCTA	60
AGCCACTTGC	CTTCTGATCG	CTGGACTGAC	TCTCTCGCCC	TCTCTTGGTG	CAGTCCTCAG	120
GAGGCTCGGT	CACACTCTCC	AAGAGCACAG	CCATCATCTC	CCACGGTACC	ACAGGCCTGG	180
TCACATGGGA	TGCCGCCCTC	TACCTTGCA	AATGGGCCAT	CGAGAACCCG	GCAGCCTTCA	240
TTAACAGGTG	ACCTCGGGGC	ACAGGGCAGG	GCACCGAGGC	AGGCTTACCC	TGGTGCCAGT	300
GAAACACGG	TCCCCCTTCC	TCCCGCCAGG	ACTGTCTTAG	AGCTTGGCAG	TGGTGCCGGC	360
CTCACAGGCC	TTGCCATCTG	CAAGANGTGC	CGCCCCCGGG	CATACATCTT	CAGCGACCCT	420
CACAGCCNGG	TCCTCGAG					438

(2) INFORMATION FOR SEQ ID NO:496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

```
GAATTCGGCC TTCATGGCCT AGGTAAAATT TGTATAACAA AAAATTAACC GTTTTAACT    60
GAATAATTCA GTGAGATTTA GTGAATTCAC AATATTGTGC AACTGCCACC TCTTTCTACT    120
TCTAAACCAT TTTCCTCATA CCAAAAGTAA GCCCCGTACC TATGATGCAG TCCCTTCCCG    180
TTTCCTTCTC TCCTCAGTCC CTGGCAACCA TCACTCTGCT TTCTGTCTCT GTGGATTAC    240
TTATTCTAAT ATTTAATTC AGTGGGAATC CCTGCCTCGA G                        281
```

(2) INFORMATION FOR SEQ ID NO:497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 570 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

```
GAATTCGGCC TTCATGGCCT ACGTAGAG AGGCAGTCGG GATGGAGGGT CGAGTTGAAG    60
ACAGGGAGGG GTGAGGAACG AGCAGAGGCC AGTTGTTTGG CCACTTGAGG GAGTTTGGAC    120
TTGTCCCAGG GGCAGTAGGG AGCCGTGAAG GGCTTCAAGC CGGGGAGGAT CATGAACATT    180
TCCCCAGAGG AGCTCAAAAT GGAGTTGCCG GAGAGACAGC CCAGGTTTCGT GGTTCACAGC    240
TACAAGTACG TGCATGACGA TGGCCGAGTG TCCTACCCCTT TGTGTTTCAT CTTCTCCAGC    300
CCTGTGGGCT GCAAGCCGGA ACAACAGATG ATGTATGCAG GGAGTAAAAA CAGGCTGGTG    360
CAGACAGCAG AGCTCACAAA GGTGTTTCGAA ATCCGCACCA CTGATGACCT CACTGAGGCC    420
TGGCTCCAAG AAAAGTTGTC TTTCTTTCGT TGATCTCTGG GCTGGGGACT GAATTCCTGA    480
TGTCTGAGTC CTCAAGGTGA CTGGGGACTT GGAACCCCTA GGACCTGAAC AACCAAGACT    540
TTAAATAAAT TTAAATGC AAAACTCGAG                                570
```

(2) INFORMATION FOR SEQ ID NO:498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

```
GAATTCGGCC TTCATGGCCT AGGTGCATGC CATCAAATAC TCTAACGAGA CATTTTAAAT    60
GAAAGACTTA AACCAGATAG GCCACAATGA ACCAAATTAG AAATCTGAAC ATGTCACCAC    120
TTGCAGCATA AAGGAATATA AAAGGGCAGA GCAAAGTCTT TTTTCCTAAG GTGAATATTT    180
CTAAGGTAAG TATTCATTTG TAAAAGTTT TTTTTCAN CANGTCTGAA NNCTTTTAC    240
CANNNGGNGA GNATTACAAC AAAACATCCC TNGGTTAAAA AAAAAAATA CCATCTTGCA    300
ATTCAGCACA CACCNGCAGC TGGTGTGCTC ATCCAACCN ATCAGTAGGC TAAGAGNATT    360
TNAAATTCCA TACATATGAG TTTAGGTATT AATGCCGATT ACACAGTACA CAGTACAGAG    420
GGAGGTCCCT ATATCCACAC ACACACACAC CCCATCCAGC ATTTACACCN AAAGCCTTAC    480
CCTCGAG                                487
```

## (2) INFORMATION FOR SEQ ID NO:499:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:

```

GAATTCGGCC TTCATGGCCT AACAAATCAA AGAAACTTTT TTCTGAACCA TTTGAAATTT      60
GCCAGCCTGA TGTCCCATCA CCCCCAAGT ATTTTAGCAT CTATGCAACA AAACATTTTC      120
TCTGACAAAA CCACATCAGA ACTCTCAAAT CAGGAAACAA ACATTGATAC ATGTCTATCA      180
ACTAATCCTG TCTTCAATGA CATTTTACCG ATTGTTCCAA TGATGTCAGC ATCACGGGTC      240
ACATTTAATA GTTGGCTCCT TCAGTCTCGA G                                     271

```

## (2) INFORMATION FOR SEQ ID NO:500:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:

```

GCACTTCTGG ATGTTGGTTC TCTTGTCTAT TTTCAACAGT CTGCAGGGAC TTTATGTTTT      60
CATGTTTAT TTCATTTTAC ACAACCAAT GTGTGCCCCT ATGAAGGCCA GTTACACTGT      120
GGAAATGAAT GGGCATCCTG GACCCAGCAC AGCCTTTTTC ACGCCCGGGA GTGGAATGCC      180
TCCTGCTGGA GGGGAAATCA GCAAGTCCAC CCAGAATCTC ATCGGTGCTA TGGAGGAGGT      240
GCCACCTGAC TGGGAGAGAG CATCCTTCCA ACAGGGCAGT CAGGCCAGCC CTGATTAA      300
GCCACGTCCA CTCGAG                                     316

```

## (2) INFORMATION FOR SEQ ID NO:501:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

```

GACAAAGACC AGCAATGGAT CACTTGGAGT CCTTTATTGC TGAATGTGAT CGGAGAACTG      60
AGCTCGCCAA GAAGCGGCTG GCAGAAACAC AGGAGGAAAT CAGTGCGGAA GTTCTGCAA      120
AGGCAGGAAA AGTACATGAG TTAATGAAG AAATAGGNAA ACTCCTTGCT AAAGCCGAAC      180
AGCTAGGGGC TGAAGGTAAT GTGGATGAAT CCCAGNAGAT TCTTATGGAA GTGGNAAAAG      240
TTCGTGCGGA GGAAAAGGA GNACTCGAG                                     269

```

## (2) INFORMATION FOR SEQ ID NO:502:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 403 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:

GAATTCGGCC	TTCATGGCCT	ACTTGTCTCA	CTCTGCATCA	TCCCTTAGTC	TACAACAGGC	60
CTTTTCTGAA	CTTAGACGTG	CCCAAATGAC	AGAAGGACCC	AACACAGCAC	CTCCAAACTT	120
TAGTCATACA	GGACCAACAT	TTCCAGTAGT	ACCTCCTTTC	TTAAGTAGCA	TGCTGGAGT	180
CCCAACCACA	GCAGCAGCCA	CAGCACCAGT	CCCTGCAACA	AGCAGCCCTC	CTAATGACAT	240
TTCCACATCA	GTAATTCAGT	CTGAGGTAC	AGTGCCCACT	GAAGAGGGGA	TGCTGGAGT	300
TGCCACCAGC	ACAGGTGTGG	TAACCTCAGG	TGGTCTCCCC	ATACCACCTG	TGTCTGAATC	360
ACCACTACTT	TCCAGCGTAG	TTCAAGTAT	CACAATACTC	GAG		403

(2) INFORMATION FOR SEQ ID NO:503:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 282 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:

GTTCGGATGA	TGGTGGCGT	GTACGCAGCT	GCTATGGCCT	GGGCCATCAT	CCCCCACTAT	60
GGGTGGAGTT	TTCAGATGGG	TTCTGCCTAC	CAGTCCACA	GCTGGAGGGT	CTTCGTCCTC	120
GTCTGCGCCT	TTCTTCTGT	GTTTGCCATT	GGGGCTCTGA	CCACGCAGCC	TGAGAGCCCC	180
CGTTTCTTCC	TAGAGAATGG	AAAGCATGAT	GAGGCTGGA	TGGTGCTGAA	GCAGGTCCAT	240
GATACCAACA	TGCGAGCCAA	AGGACATCCT	GAGCGACTCG	AG		282

(2) INFORMATION FOR SEQ ID NO:504:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 222 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:

GAATTCGGCC	TTCATGGCCT	ACTGAGAAAA	AAAATCAAAT	CTAATTTTAA	AATGAAGGTA	60
TTTAAACCA	TGGCACAAGG	GAGCCTTATT	TATGGAGCTG	GTGGGAAGCC	AGGATGTTTC	120
CAATCCGCTG	CTCTTACAGG	AGCCTGTGCC	TCGCCAGTTC	TGTGCTGCAG	TGGGCAGCCA	180
ACTGAAGTGC	ATGAGTCAAA	TGCACGAAGC	AGCAGACTCG	AG		222

(2) INFORMATION FOR SEQ ID NO:505:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:

GAATTCGGCC TTCATGCCCT AGTGGTGAG TTTTTCAGGA TTGTAGAGAT GCTAACAAAT	60
TACAGGTTCT CTCATGCAAA CACTTTGCTA GGAATTATAT ATATCAAGTT TATATTTGGC	120
AATCAGGCTT TAGAAGCAGA AGGTCTAGCT ATCTCAAACCT ACCACCTACC TCCCTCACCA	180
AAGCCGCTCG AG	192

(2) INFORMATION FOR SEQ ID NO:506:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

GAATTCGGCC TTCNTGGCNT AGTAAAATTG TTAAAGTTGA CAGGATCAGT TTTGGAAGAT	60
GCTTGAAGG AAAAAGGAAA GATGGATATG GAAGAAATTA TTCAGAGAAT TGAANACGTT	120
GTCCTAGATG CAAACTGCAG TAGAGATGTA AGACAGATGC TCTTGAAGCT TGTAGAACTC	180
CGGTCAAGTA ACTGGGNCAG AGTCCANGCA ACTTCAACAT ATAGAGGNGC NACACCAGAA	240
AATGATCCTA ACTACTTTAT GNATGNACCC ACATTTCATA CATCTGATGG TGTTCCTTTC	300
ACTGCAGCTG ATCCAGATTA CCANGAGAAA NTCCAAGAA NACTTGAAAG AGANGATCCT	360
CGAG	364

(2) INFORMATION FOR SEQ ID NO:507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

GAATTCGGCC TTCGATTGAA TTCTAGGACT TGACAGAATT CGAGTTATCC TTCTCAGAAC	60
ATGTGCAGAG TCTCTTTTGG CCTCACCATG TGGTCCTGTG CTCCTTCAGG TGGGAGTTT	120
GGGGCCTCCA GGGCAGCAGG CACCACCTCC ATATCCCGGC CCACATCCAG CTGGACCCCC	180
TGTCATACAG CAGCCAACAA CACCCATGTT TGTAAGCTCCC CCCCAAAGAC CCAGCGGCTT	240
CTTCACTCAG AGGCCTACCT GAAATACATT GAAGGACTCA GTGCGGAGTC CAACAGCATT	300
AGCAAGTGGG ATCAGAGCAA TCTCGAG	327

(2) INFORMATION FOR SEQ ID NO:508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

GAATTCAGTG	AGTGGGCATG	GCTGATCTTG	TGCAAATTAA	AAGTTATGGG	GCATAAGAAT	60
AGCAAAAGTT	GAACCTCTTT	TAAAAAGGAA	AGTACCCTGA	GAGCCAGTAT	TGGTTGAGGC	120
TCTTCAGTAT	CCCCAGGTTG	GCAGCACTGA	GAACCGCAGG	AACGGCCTGT	TGTTACAAAA	180
AGGAGATTGA	CTCAGCTGCC	CTTGGTGCAT	CTGACTGACT	ATGACTGCTG	AGAGATTCCA	240
AGGACCCTTA	ATGCCAGGGC	TAACCTCTCC	ATGTGCAGTG	AGACCTCTGG	AGGAAGTGTC	300
ATCCTCTGGC	TTTGTGTGGT	ACTCATTATG	GTGCAGTGCG	GGCATGAAAT	GAAGACACAC	360
AAATAGGCTC	GAG					373

## (2) INFORMATION FOR SEQ ID NO:509:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:

GAATTCGGCC	TTCATGGCCT	ACTCTTCCTG	GCTCCTTCTC	AGCCTTGTTG	CTGTAAGTGC	60
TGCTCAGTCC	ACCATTGAGG	AACAGGCCAA	GACATTTTGG	GACAAGTTTA	ACCACGAAGC	120
CGAAGACCTG	TTCTATCAAA	GTTCACTTGC	TTCTTGGAAT	TATAACACCA	ATATTACTGA	180
AGAGAATGTC	CAAAACATGA	ATAATGCTGG	GGACAAATGG	TCTGCCTTTT	TAAAGGAACA	240
GTCCACACTT	GCCCAAATGT	ATCCACTACA	AGAAATTCAG	AATCTCACAG	TCAAGCTTCA	300
GTGCAGGCTC	GAG					313

## (2) INFORMATION FOR SEQ ID NO:510:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:

GAATTCGGCC	TTCATGGCCT	ACTTGAACAA	TTAAATATA	GGAGAAGACT	ATTTTITAGA	60
AATGTTTTC	GTGCGCAACT	TGTTAAAGCT	TTATAGCACT	TTGCATATTT	TGGAGAATGT	120
CAACTATATT	TTTATCAGAG	CTGATTGTG	CCAGTGGAAC	AACAGTGCGG	TAGACATCGC	180
CCACAAGGTT	CTGCATACTC	GAG				203

## (2) INFORMATION FOR SEQ ID NO:511:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:

GAATTCGGCC	TTCATGGCCT	ACGTGGTATT	AAGGAGACAA	TCTGAGGCAT	TCCCACCACT	60
CAATTTGACA	TGCGGTTGGC	AAGGTTTCCTC	TTCCCTTCCC	ACTTTAGATC	GTGCCCTGTC	120

CCAGGTCAGA CCCGAAAGAT TCATAGGCAC ACTTACAGCC TTCATAGTCT CAGCCATAGT	180
CATCCTAGCA ACTGCTAGTG TGGCTGTAGC ATCTATTACT GAATCAGTAC AACAGCTGC	240
TTTTGTAGAT AATTTGGCCA GAAATGTTTC TAATGAACTT CTCTTACAGC AAGGTATAGA	300
TCAAAAGATT CTTGCACATC TGCAAGCCCT CGAG	334

## (2) INFORMATION FOR SEQ ID NO:512:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:

GAATTCGGNC TTCATGGCCN AAAGCTCTNG AAGGAGTATT AGAGTACAGA GTCTGAGNCT	60
NTGANAAATG GTGGTCAGAA GCCNTCTTCA TCAGATANAT TTCTCAGATG TGCCCCCTTC	120
GCGGCAGAGG NGGATATTCA TCTCCTAGTT CATGTTTCTG AACATGTCAG TANGCAGATN	180
ANTCACTACC AGTATCTGCT TCTACTTTTC CTGCATGAGT CACTTATCCC TGCTTTTCTG	240
GAACNTAAGG AAAGATGTAG AAGCTGTAAC TGGCAGTCCT GCTAGTCAGA CATCCATTTG	300
TATTGGAATT TTACTTAGAA GTGCAGAACT GGCTCTTTTG CTCCATCCAG TGGATCAAGC	360
AAATACTCTT AAGTCTCCTC TTTCTGAAAG TGTGAGCCCA GTGGTACCTG ANTATTTGCC	420
TACAGAAAAT GGGGATTTTT TGNCCCTCAA AAGAAAACAA ATTAGTAGGG ATATAAATAG	480
AATTAGAAGT GTAACGTGTA ATCATATGTC AGACAACAGA TCTATGAGTA TCTCGAG	537

## (2) INFORMATION FOR SEQ ID NO:513:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

GAATTCGGCC TTCATGGCCA AGGTGCTTAA TATTAACAAA AAAAAAAGTA TATCCAACCA	60
CAGATATACA GTTCTGCCTT TTTTCTCTT TTACCTAAAT ATACTCCATA AACAGTTTCC	120
ATGTTGTGTA ATATCTTCAT GTTCTACTT TTCAGTGATT GCTTAAATGT CCATTGGGCT	180
GATAGGTCAC AGTTCGCTAA CCCATCTCAT TGTTGTTCAT TGGGATCTCC ACTTCCCTC	240
GAG	243

## (2) INFORMATION FOR SEQ ID NO:514:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:

GAATTCGGCC TTCATGGCCT AGTCTCAAAA AAAAAAAAAA GATTATCCAC AAATGCAGTG	60
GNCCCTGGGA CAAGCCCTTT AAAGGAGTCA TNGAGAATCG TCTGTTGCTC ACAGCATCAA	120



TCNGGTATTT AGTTCTCAAG CTGAGGATT CTAGTTTTCG TCAGAGGGTC GGGTTCAGTC	180
TCTAAAAGAC GCTCTGAAAG CAGACCAGGC TGTTTCTTG GAGCTTTTCA GGTTAGATTC	240
TCATGTGTGT ATCTTCCATC TACCACGATT ATTTGGCTAC CAGATGCCTT AGCAAGCTGA	300
ACAGTGAGCT CAGAAGTGCC ACCATCTATA GTAACATTCT CGAG	344

## (2) INFORMATION FOR SEQ ID NO:515:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:

GAATTCGGCC TTCATGGCCT AAGAGTATCC GCTTACAGAA AAGACACTTC ATCACCTAGC	60
ACTGATTAT GCAGCTTTGG TTTCATTTGG GCTAACTCT GAAGAACTGG ATGTAAAGCT	120
TATAATTGCC CCAGGAGTAG AAGCAACTGC CTTGATAATT CGACAAATTG CTGACCACAG	180
TTTAATGACC TCAAAGAGAG ATCCTCATGA ATGTTGGAT AAATCCTGGC TTAAAGTTTC	240
ACCATCTGAG GAAGAAATGT ACTTACTTGA TTTTCCATGT ATTAACCCAA TCGTGGCTCG	300
AG	302

## (2) INFORMATION FOR SEQ ID NO:516:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:

GAATTCGGCC TTCATGGCCT ATAGGCCATG AAGGCCGGCC TTCATGGCCT AATCCATAAA	60
AGGCTTTTGA GATGTCTCTG CTGAAAATAA ATGAGCTCT AGTAAATGTT AGAGTTTTCG	120
CTAGTAGAGT TTTGATGCTT TTTGTCTTG TTCTACTACT GAGCTTGAC CTAGGATGCC	180
TTCTTATAGT GCCATTCAAC ATGCAAGTTT CTTTTCTGG GGCTGTGTGT CCAGGTGACT	240
TTATGAGTTA GGCTTTGGCA AATGCCAGAC TTGTTTCATCC TAACACTAGA ATGTAGGGAT	300
CCTGCATTCA GCATGACCCT CGAG	324

## (2) INFORMATION FOR SEQ ID NO:517:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

GAATTCGGCC TTCATGGCCT ATAGGCCANG AAGGCCGGCC TTCATGGCCT ATAGGCCATG	60
AAGGGTTGGT TGTGTTTTCC TAACAATGAA TAAGACAGAA ACCCTTGATA GCTAAATTCA	120
TCTGCAGTCA AACTAAGTTT TGCAGTGTCT TTTTAAGAGC CAGGCAATTC TACCACAAAA	180
TAAAATATAT TTTTAAATC CACATTACTA TACCACTGAC AAGTCTTTAC TTCAGAACTC	240

ATCATTCAGA AATGTGTAGC TGCTTCCAGA GTGTGTCTAA TACTGTTGGA ACAGGCGTTT	300
CAGAAAGAAA TGAGAGGCC AGTCTCAGTA ACTCCATGAA GGGTGCCGAG CTCCTCTGTT	360
GAGGATTTGG CTTGTGAGAG GCAATGTTCC TATCATTTGC CAATTTGGCC TTTGTTATTC	420
CCACATTGGC TCGAG	435

## (2) INFORMATION FOR SEQ ID NO:518:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

GAATTCGGCC TTCATGGCCT ACCAGGTTGG CCAGGCTGGT CTCGAACTCC TGACCTCAGG	60
TGATCTGCTC ACCTCGGCCT CTCAAAGTGT TGGGATTACA GGAGTGAGCC ACCGCACCGG	120
GCCAAAAAAT CCAATTTCTT AGAGATTAAA TAACCTTCA GGATTATCAA AGGAAATAAT	180
TAGGGAAGG TAGATGTTCT GTCCAGTAA GAGAAGAAAG TGGTCCAGAA ATTTTATCTC	240
CCATCAAATG ATCCATTTTA CTTAAAGTATT AAACCAAGTG ACATTCTTCA GTTTAACTCT	300
GATAAATGAA TCATATTCCT CTTGAAAAT AACTTTTGTA TTTCGTGCTC TAAAAAGAGA	360
ACCACCCCTC GAG	373

## (2) INFORMATION FOR SEQ ID NO:519:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

GAATTCGGCC TTCATGGCCT AAACAATTAA TTGTGGGTGT CTGAGGGGGA AGGTCGCAGC	60
TTTGGGCAGC TTTGAGAAGC GGTACAAGAG TTCTGTGCCT GTGTGTCCAG CCCTGGAGCC	120
AGCCAGTGCA TTTATTTTAA GCTCTTAGAA GCAACTCCTT GGCCGAGGAA TGCCTGACCC	180
CTGAGATGGG TCCACGCATC TCTCTACACT TCCTTCTCTC CGTGGGATAC TGGACTCGTG	240
CCTCTGCGCC CATTCTCTTC TCACGCATAT CCATGAGCTT TAATTTCACT TTCTGATCAG	300
GGTACGTCCA TAAAGCCAGT ATTACACTTA AATGAAGTAT TCTTTTTTGT AATCGTTTTT	360
TTTAGAAGGT AAACAAATTT AATAAAGCTA TCTCGAG	397

## (2) INFORMATION FOR SEQ ID NO:520:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

GAATTCGGCC TTCATGGCCC ACATGAATCT NGTAATTTGT GTCCTACTTT TGTCCATTG	60
GAAAAATAAT TGCATGACTA CAAACCAAAC CAATGGATCT TCTACTACAG GAGATAAAC	120

TGTGGAATCA ATGCAGACAA AATTGAACTA CCTTAGAAGA AATCTACTCA TTTTAGTTGG	180
TATTATCATC ATGGTTTTTG TCTTTATCTG TTTTGTGTAT CTCCATTATA ATTGTCTGAG	240
CGATGATGCG TCCAAAGCAG GAATGGTCAA GAAAAAAGGC ATAGCAGCCA AGTCATCTAA	300
AACATCATTC AGTGAAGCCA AGACAGCCTC TCAATGCAGT CCAGAAACAC AACCCATGCT	360
ATCTACTGCA GACAAGTCAT CTGATTCATC GAGTCCAGAA AGGGCATCCG CACAATCCAG	420
CACAGAAAAA TTAATCAGAC CCTCAAGTCT ACAAAGCCA TCCAACCTCG AG	472

## (2) INFORMATION FOR SEQ ID NO:521:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:

GAATTCGGCC TTCATGGCCT ACACCTCTTC TTAGGGCTGT TTTTAAAC ACAATGATAT	60
TCTAAGGAAC AAGAGGTTGG CTATGGACTT TTGTATACCC ATGCCTATCA TATTTCGCTA	120
AATGTTTGAT TATATAGAGA CATTCTTTG GAACTTTGAG CTGTGTGAAG ACAACACAAA	180
CCTGGCCATT CATGGCTGAC AGAAGGTTGG CCCTAACCCT GCTCAGGCCC ACACAGATTG	240
TGTAATATTC TTTGGATCTG GCTCTAGTCA GCAAAGTCTT GGTGTTGTAG GATACAGGTG	300
TCTTCATGCA TTCCATTTA TACTCGAG	328

## (2) INFORMATION FOR SEQ ID NO:522:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:

GAATTCGGCC TTCATGGCCT AGAAAAAGAA AAAGTAGCTG ATGAAGATGA TGTGGACAAT	60
GAGGAGGCTG CACTGCTGCA TGAAGAGGCT ACCATGACTA TTGAAGAGCT GCTGACACGC	120
TACGGGCAGA ACTGTCACAA GGGCCCTCCC CACAGCAAAT CTGGAGGTGG GACAGGCGAG	180
GAACCAGGT CCCAGGGCCT CAATGGGGAG GCAGGACCTG AGGACTCAAC TAGGGAACT	240
CCTTCACAAG AAAATGGCCC CACAGCCAAG GCCTACACAG GCTTTTCCTC CAACTCGGAA	300
CGTGGAAGCTC GAG	313

## (2) INFORMATION FOR SEQ ID NO:523:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:

GAATTCGGCT TCATGGCCTA GCGTTGTGTG CATGCGAGCG CTCCTGCAGG CGTGTGCATG	60
GGGCCAGGTG TGCACGTGGA TGCCCGGGTG AGTGTGTGTG CATGCACGTG TGTGCACGCA	120

TGTGCACATG CCTCCAGCCC CACCTTCCAA CCCCTCAGTG CCCCCAGGAC AGGGGCCCCCT	180
CTTAGCTATC AGGGTATGGC CGGACCGGCC CTTCTGCCC AGCANGTTGC AAGCACTTGG	240
CCAGGCCGGC CCTCCAGGNT GCTGCTGCGT GGGGGCCCCG GTGCCCCCAG GTCCATGCAG	300
ACTGGGGATT CGGTGGGGAG GGGCGCTTCT AAGGAACCAA ACTGACGCTC ACTCTGGGCT	360
TCCAAGCAC CCTTAGCACG GAGCCACCC CTAGCTCGAG	400

## (2) INFORMATION FOR SEQ ID NO:524:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:

GAATTCGGCC TTCATGGCCT ACCCACCCTG TAGTCAACCC CACTCGTACT GTAGCGAGAC	60
AAAAACATGC CATTGTGAAG AAGGGTACAC TGAAGTCATG TCTTCTAACA GCACCCCTGA	120
GCAATGCACA CTTATCCCCG TGGTGGTATT ACCCACCATG GAGGACAAAA GAGGAGATGT	180
GAAAACCAAGT CGGGCTGTAC ATCCAACCA ACCCTCCAGT AACCCAGCAG GACGGGGGAG	240
GACCTGGTTT CTACAGCCAT TTGGGCCAGA TGGGAGACTA AAGACCTGGG TTTACGGTGT	300
AGCAGCTGGG GCATTGTGT TACTCATCTT TATTGTCTCC ATGATTATC TAGCTTGCAA	360
AAAGCCAAAG AAACCCCCCT GCCTCGAG	388

## (2) INFORMATION FOR SEQ ID NO:525:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:

GAATTCGGCC AAAGAGGCCT AATTGAATTC TAGACCTGCG TCGACCGAAC CGAGTTGTAC	60
ATTTTTTTTG TGATGGGTTA TTTTATTATT TAATTATTAT TGTGTTTTTG GTTTTTTTTT	120
GGTTGGTTTT NGATTTATGA CAATNCCACT CTTGGCCCCA GTTGTCGTCC TGCTACTCCC	180
TCCCCTGTCC ATCACCCTGG CTCCCAGACC AGGCTCAGCA ACACATTGAG TCTTGGGTTC	240
CAGGAACCTT GCCAACCTCA ACCCTCCAGC CCGTGCTCCA CTGGCTATGG CTCAGACCAA	300
GGGCTCCTCC TCTCCNTCT TGCCCTATGG AACAGCCCGG GTGCTCCAAG GGGGCCAGGA	360
GGGCATGGCT TGGCTCCCAA GATAAGGGGT CCGGGGCCAG GACACCCAGG CAAGGTGGCC	420
CCTCCCTGCC TAGCCCCCTT CCCCCACCC AAAGTCGAG	459

## (2) INFORMATION FOR SEQ ID NO:526:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:

GAATTCGGCC TTCATGGCCT ACAACCTGGA AAATTCTCTG ACTTAGAAAT TTAAACAAAA	60
CCCTCCCCTT TCATTGAATC TCCATTGTCT GGAGTTTGCT TGTTTTAATC TAGCCTGTTC	120
CTCCACTATG GGCTCCCCTT CAAACTATGC CCTGCTTCAA CTAACCCCTA CTGCTTTTTT	180
GACAATTCTA GTACAACCTC AGCACCTGCT TGCTCCAGTT TTCCGGACAC TATCTATCTT	240
GACTAATCAG TCTAATTGCT GGTATGTGA ACATCTAGAT AATGCAGAAC AACCCGAACA	300
CCTCGAG	307

## (2) INFORMATION FOR SEQ ID NO:527:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

GAATTCGGCC TTCATGGCCT ACCAATACTA AGCTTATTTT ATTGTAATAC AGTTATTTGT	60
ACCACCTTAG AGCAATCTTT TGAAGAACAA GAAACACATA TTGAGCCACC ACGCCAGCC	120
TTTTTTCAGT TTATTTTAA TCTTTTGCTG TTCATTGGCT CATTCTGTGT ATAAGCATGT	180
TAAATTTACC CAAATATGAA AATAGCCTCC CCTTGGCCCT GAACTCCTCT ACAAGCAACT	240
ACCTCATGAT TTTATCTCTT TATCCTCAA TTCTTTGGAA TATAATTTAT ACTTGTTTCA	300
TCCCTACCAC CCTCGAG	317

## (2) INFORMATION FOR SEQ ID NO:528:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:

GAATTCGGCC TTCATGGCCT ACAGCAGTGT GCTTTCATCC AGTTTGCCAC ACGGCAGGCT	60
GCAGAAAGTGG CTGTGAGAAG TCCTTTAATA AGTNGATTGT AAATGGCCGC AGACTGTATG	120
TGAAATGGGG AAGATCCAG GCAGCCAGAG GAAAAGAAAA AGAGAAGGAT GGNACTACAG	180
ACTCTGGGAT CAAACTAGAA CCTGTTCCAG GATTGCCAGG AGCTCTTCCT CCTCCTCCTG	240
CAGCAGAAGA AGAAGCCTCT GCCAACTACT TCAACTTGCC CCCAAGTGGT CCTCCAGCTG	300
TGGTGAACAT TGATNTGCCA CCGCCCCNTG GCATTGCTNC ACCCCCACCC CCAGNTTTTG	360
GGCCACACAT GTTNCACCA ATGGGACCAC CCCCTNNNAC TCGAG	405

## (2) INFORMATION FOR SEQ ID NO:529:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:

GAATTCGGCC TTCATGGCCT AAGAAACCAA ATTAGCAGAC GGATAGAATA TAAAGCAAGA	60
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GGCAATACTT ATAGTGTATT AAGAACTTG CTAGACCCCA TCCAAATTAC TCAGTCTACT	120
GTTGGTTGAT AGAATTACTT TAGGAAGAGT ACGTTTTTGC CTTGGAAATA CACTGGAAGT	180
GGTACCAAAC AAATCTAATA AAATGATGTT AAAGAGATTT GCAGTAATTT TTATCAACTT	240
TCAGTTTGCA AACTTTTATA AAGATATGAA CGGGACACTC GAG	283

## (2) INFORMATION FOR SEQ ID NO:530:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:

GAATTCGGCC TTCATGGCCT TTCTATAAAT GAGTTCTTTA TAAGAAGCTT GTATCATTCT	60
CACAAATTAA AAATAATAAT ATTTTAGCAA GCTATTTTTT AAATATAATT TAAGCCCACA	120
CTTCCACATT TGGGGTAAGT GATAATTTTT TCCTCTGAAA GACAACAAAT ACTAACACAG	180
GCCCAGACTT GGCTTTTGTG AGTCAATTAG TGATCCGAAG GTGAGTGGTA TTTAAACGTA	240
TGATGAGGGT AAGATTTGAT TTATTTTACA TATATATCTT CTGGTATCTG TGTGTGTGTG	300
TGTGTGGTGT GAAGCTCGAG	320

## (2) INFORMATION FOR SEQ ID NO:531:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:

GAATTCGGCT TCATGGCTTG GGGGTGACAG TTAATATATN CGGTCATTTT AGATTGCTTC	60
CACTAATATT GGTATTATCCA TATTATAAAA TATTTTAGTG AGTATAAAAT TGTCTGCATT	120
CATAAAGATG CATAAAATTA ACTACAGAAC CAGCTTGAGT AATGCTTTTC TCTTCTTTTC	180
TTCTTGTCAA TCAGATATTA TCTTTATACA TTGTTTTAGA GTATACATCT ATCAAAATGC	240
AACATTGTTG AAGGATATGT AATTTATACA GCAAACGTGT AATGGATAAA AATGTGCAAA	300
AACAATCCTT AAAGTATTGT ATTTGAACNA AAACAATCTT AAACCACATA ATCTGAAAAA	360
AAGGGGTACA TATTTTACCA AATATACTAA TCCATACAAG ACTGCTTGAG AAAAAGAATA	420
TGCCACCTAC TCGAG	435

## (2) INFORMATION FOR SEQ ID NO:532:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:

GAATTCGGCC TTCATGGCCT AAGCCATCAG ATTGAAATTA ATTTAGACAG GAAGAATCTA	60
TATAAATTTG ATGCATAGCA AACTCTGACA TAATTTGGTT TATTTTGAAG TCTGGCATAT	120

TTTTCATCAC TTTTATTTT ACGGGTAAAT CATAATATAT CATATTTTCA ATAAAAGTAT	180
TTTCTTAAAA ATCTGCCATT TGCTTCACAG ATTTTAAATC TTCTAACAGA AAAAGAAGTA	240
AATATTGTTT TGCCAACACA GTCCATTGTT CCAAGAACTT TTGTGCTTAA ACCAGGAATG	300
GTTCTGTTTT TGGGTGCTAT AGGCCGCATA GCCCTCGAG	339

## (2) INFORMATION FOR SEQ ID NO:533:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:

GAATTCGGCC TTCATGGCCT AATGTGCTCC AGGAGGCGCT GGGGGATGGT GACCTCCCAA	60
GGCGGGCAGA NGACTTCTGC CGTCAGGGTC GCCTGCTGCT GAGCCTGGGG GATGAGGCGG	120
CGGCCGCAGG GTCTGGATCC CCTGTGCCGT CGCCTCTTCC TTTTTCGACG CCTCCGCCGC	180
CGCCTGAGGA GCGGAGCTAG CCGGGAGTTA CACCGCCACC GCCAGGATGG ATAGAATGAC	240
AGAAGATGCT CTTGCTTGA ATCTGTTGAA GCGGAGCTTG GACCCAGCAG ATGAGCGAGA	300
TGATGTCCTG GCAAAGCGAC TCAAATGGA GGGGCATGAG GCCATGGAAC GTCTGAAAT	360
GTTGGCATTG CTCNAAAGGA AGGANTTGGC AAATCTTGAG GTGCCACATG ANTTACCCAC	420
CNAACAGGAT GGCAGTGGTG TCAAGGGCCA TGAAGAAAAA CTTAACGGGA ACAACTCGAG	480

## (2) INFORMATION FOR SEQ ID NO:534:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:

GAATTCGGCC TTCATGGCCT ATATGATTTT TTAATCTATG ATGGTTTATG TGAATAGGAT	60
TTTCTCAGTT GTCAGCCTGG GCGACAGAGC GATACTCCAT CTAAAAAANA GNAAAAAANA	120
GAGGTGACTA GGCCATGAAG GCTCTGTCCT CACAGATGGA TTAATGCCAT TGTGTGGGA	180
GTGGTTTTCT CATGAAGGA TGAGCTTGAG CTTGGCCCCC TTCCTTCTCC CGCCTCATTC	240
CCCTCTATGT NGCCCCTATG ATGCCTAANG CCATGTTATG ATGTGGCAAA AAGGCCCTCG	300
CCAGATGCCA GCCCCTTGAC CNTGGAATTC CCAGCATCNA GAACTGTGGA CCNAATGNAT	360
GTTTTTTCCT TATAAANTAA CCNGCCACNG GTATTTTGT AAAGCNGCAC CNAGCAGACT	420
CGAG	424

## (2) INFORMATION FOR SEQ ID NO:535:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:

GAATTCGGCC	TTCATGGCCT	ACGTTGACTT	AATCAGAGGG	TCAACATTG	CCAAAGCAAA	60
ACCTGAAATT	CCATGGACAT	CTCTGACTCG	GAAGGGGCTT	GTTGAGTTG	TATTTTTC	120
ATTGTTGAGC	AATTGGTGGA	TTCAGGTAC	CTCTTAAGA	ATCTTGTTT	GGCTGTTACT	180
ACTTTATTTT	ATGCAAGTTA	TAGCAATTGT	CTTATATTTG	ATGATGCCTA	TTGTGAACAT	240
AAGTGAAGTA	CTTGGACCCT	TGTGCCTTAT	GCTACTCATG	GGAAGTGTCC	ACTGTCNAAT	300
TGTGTCTACT	CAGATAACAA	GACNTCAGG	AAACCTCGAG			340

## (2) INFORMATION FOR SEQ ID NO:536:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:536:

GAATTCGGCC	TTCATGGCCT	AGGCGCTCGC	TGAGGCAAAA	GGAGGCGCTC	GGCCCGCGGC	60
CTGACAGGGA	CTTAGCCCGC	AGAGATCGAC	CCCGCGCGCG	TGACCCACAC	CCCACCCACT	120
CATCCATCTA	TCCACTCCCT	GCGCCGCCCT	CTCCACCCCT	GAGCAGAGCC	CCCGAGGATG	180
ATAAACACCC	AGGACAGTAT	TTTGCCTTTG	AGTAACTGTC	CCCAGCTCCA	GTGCTGCAGG	240
CACATTGTTC	CAGGGCCTCT	GTGGTGCTCC	TGATGCCCCCT	CACCCACTGT	CGAAGATCCC	300
CGGTGGGCGA	GGGGGCGGCA	GGGATCCTTC	TCTCTCAGCT	CTAATATATA	AGGACGAGAA	360
GCTCACTGTG	ACCCAGGACC	TCCCTGTGAA	TGATGGAAAA	CCTCACATCG	TCCACTTCCA	420
GTATGAGGTC	ACCGAGGGTA	CTCGAG				446

## (2) INFORMATION FOR SEQ ID NO:537:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:

GGCAAATTAC	ATCACCAAAT	CAGCATATTC	TCCACTGGAA	AGGAGAGGCC	CACATAGCCA	60
AATTATAATC	TGCAGGTTTC	TGAGCCAGTG	TTAAATCTGA	ACAGAGAAAA	GATTTTTC	120
TCAATTGGCA	AATTTTAATG	ACATCACTCA	TTGATACCCC	AAAATCTCCA	GTTCTTACCA	180
AGCTTGGCCT	TGCCAGTGG	TTCCTCTGTT	CCCTCAACAA	TGTTTCATGG	NATCTAACAA	240
CTTCCCTACC	CATAACCTT	CTCAGCTTTC	ATGGTGAACC	AAGCCTCCTC	TGTCGCACTA	300
ACCTTCCCAG	CTTTCATGGT	GAACCAAGCC	TCCTCTGTCC	CGCTATTCTC	GAG	353

## (2) INFORMATION FOR SEQ ID NO:538:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:



GAATTCGGCC	TTCATGGCCT	AAGAAGGAGN	AGCAAGCGGA	TTTCAGAGAG	GTGTTCTTC	60
AGAAAAAAT	GGTTATTTCT	TTGAACTCAT	GCCTGAGCTT	TATTGTTTA	TTGTTATGCC	120
ACTGGATTGG	GACAGCATCA	CCTCTGAATC	TTGAAGACCC	TAATGTGTGT	AGCCACTGGG	180
AAAGCTACTC	AGTGACTGTG	CAAGAGTCAT	ACCCACATCC	CTTACTCGAG		230

## (2) INFORMATION FOR SEQ ID NO:539:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:

GNGAACCAGA	GATCCCCATA	GATGGAACAG	AATTATCCCA	CTACCGTCAG	CGTGCCCTCC	60
TGCAATCACA	GCCAGTTCGC	CGGACGCCTC	TCCTCCACAA	TTTCCTGCAC	ATGCTGTCCT	120
CCCGCTCTTC	TGGCATCCAG	GTGGGAGAGC	AAAGCACAGT	GCAAGATTCT	GNTACCCCTT	180
CACCCCCACC	GCCTCCCCCT	CAGCCCTCCA	CGGAGCGCCC	CAGGACTTCC	GCTTACATCA	240
GGCTCCGACA	GCGGGTCAGT	TACCCACAG	CTGAGTGCTG	CCAGCACCTT	GGGATCCTGT	300
GCCTTTGCAG	CCGCTGCTCT	GGCACTCGAG				330

## (2) INFORMATION FOR SEQ ID NO:540:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:

GAATTCGGCC	TTCATGGCCT	ACTCCGACTT	TCGTTCTTGA	TTAATGAAAA	CATTCTTGGC	60
AAATGCTTTC	GCTCTGGTCC	GTCTTGCGCC	GGTCCAAGAA	TTTCACCTAG	TTACCCCTCTA	120
GAATTATTGC	ATTGGGGCCA	GGTGGTGTCT	AGTACAGTTT	TTTACTTTGG	AGAATTTATT	180
GAAATTTTCT	TTGGCTGAGA	ATGCCCTTCAG	TGTTTGTGGT	TATTCCTTGG	ATACTTGCAA	240
ATCGATTGTA	TTTTCTCTGG	GACACGGGGT	TTCAGATAGA	TCAGTTAAAT	GAAGCTTGAT	300
TATATCGTAT	TTACAGTCGC	ATGCCATGTG	TCTTGTCTGT	TGGACTGTCA	GGTCTCAAGA	360
GACGGGCTTG	GGTTTCCCTG	TGTGGCTGCT	GCCTTGCCCC	TTCCCCGATC	CACACTCGAG	420

## (2) INFORMATION FOR SEQ ID NO:541:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:

GTGGGCAAAG	AAATGAAGTA	CATTAAGGAG	GCCTTTTTTT	TCCTCCAATG	GCTGTTAGAT	60
TGTGTATTGC	AACCAGGAGT	TGTCAAGCTC	CTGATCCTAA	TCCAAGCTGG	GGACTGTGGT	120
ACAGTGTGGC	CAGTGCCTT	GCCAGCTGCC	TTACCAGGCA	GGTCTCGCAT	CTGCCATTGT	180

CATCCCATTG GAATCAAGTT GCAAGCCAGT GAACTTGCTG GGGTGTGCCC AGGTCAGAAC	240
AGTTACAGCT TAAAAGCCTT TGCTGCCCTT TTTCAGATCC TGTTCCCTGGG AGAGTCTCCC	300
ACACTAAGTT CAGTGTGGGT ACCAGCTGTG GTGAGGGTGT GCTGCCACTG CAGCTGCTGT	360
CTGGGCATCT GTGTTAGGGC CAATACTTCA AGAAGTGTGA GTCATTGTGA AGTGACTGTA	420
GGCAGCTGGG AAATAACAGC TGTGAACAGA GAACAACG AG	462

## (2) INFORMATION FOR SEQ ID NO:542:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:

GAATTCGGCC TTCATGGCCT ATGGGAGATA GGGGACTTAA TTATTTGTG GGTTTTTTCT	60
TTTTTAGGTC TTAGGAAGGT CTTTGTTCCTA TAGGTATCTG TATAATACAA TTTTATTAGG	120
TGTAATAGAG ACAGTTTTGT GGAAACAGAA TGCTGACACT GATTAAATTT AAGGTGTATA	180
TATGTTTAGT CTTTGAGATG ATCTGTATGC TACATGTAGG TGTACATTGT AATTTTCTGG	240
CTTGTAATTT TTTGTATCAT ACTCTGTTTC GGGAAATTGC AAATGCCTAT GACCAGCCTA	300
TGACATCTGA ACCATACCAA CTGACCTTAG AAACAACGAC ACTCGAG	347

## (2) INFORMATION FOR SEQ ID NO:543:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:

GAATTCGGCC GCCTAGCAAA AGTGAAAAA TAAATAAAAC AAGCCACAGA TTGGGACAAA	60
ATATTTGTGA AGGATATATC TGATTAAGAA GTTATATCCA GAATATATGA AGAACTTTCA	120
AAACTAAAGA AAACAATTCA TTTTCTTAAT TGGGCAAAAG ATTTAAACAA ATATTTTACT	180
AAAGAAGATA TCCAGATAGC AAATAAACAC ATGATATTCA CCGAAATTAT TAATTAGGAA	240
AATGCAAATT AAGATGAATA TCATTATATA CCTACTAGAA TGGCTATATT TTAAAAGTTT	300
GACACTGCCA ATTACTGGTA AAGATGCAAA TCAGCGGAAG CTCGAG	346

## (2) INFORMATION FOR SEQ ID NO:544:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:

GAATTCGGCC TTCATGGCCT ACTTTCTTCC TACATTAGTG GCATACTCTG AATGACCTAG	60
TGAACAGACT GAGAAGAGGC CTCTGAATTG CAGAGTCTCG TCTGTAGGAG AAGGTTTCAGG	120
AGAGTATTGA ATTTTAGGGA CTAGAATCCA TCTTACCTAT GCTGTTGCAA TCGCATGCTG	180

ACTGGAAGTG TGGGAAAGAG ACTTACAAGT AAGGACATGG GTTTGTTTTG TTTTGTGTTT	240
TTTGTGACAG AGTGAGACCC TGTCTCGNAA AAGGAAAAAA AGTAATAGAA CATTAAATAC	300
AGTATCACAC CATTATGGT TAAAAAGNA AAAAGACAAG ACACTATATG AAGTGAGTGT	360
CTTTTAAAGT TAAAAAATT AAATGAAAAC AAACTCGAG	399

## (2) INFORMATION FOR SEQ ID NO:545:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 367 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:545:

GAATTCGGCC GCCTCCATCT CCCTGGCCAT GTTCTTCTTG AAGACCCTGA CAGTGGCTTC	60
TTCTTTGTGG CAGCTGGCCA ACAGCCAGAC CCTGACAGCC AGCCCCAAG CACCTGGGTC	120
CCCAGAGGAT TCTGAGGGTG TCCCCCTCAT CAGCCTGCCC CGCGTGCCAC AGGGAGGGAG	180
TCAGCCTGGG CCCAGCCGGG GATTAAGTCT CATGTCCAGT CAGGGCAGTG TGGACTCAGA	240
CCACCTAGGT TATGATGGTG GCAGCAGTGG CTCAGACAGT GAGGGTCCCA ATGACACCCT	300
TGGTGAGAAG GCCCCCTTCA CATTGCGGAC TCCACCTGGG CCAGCACCTC CACAGACTTC	360
ACTCGAG	367

## (2) INFORMATION FOR SEQ ID NO:546:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 455 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:

GAATTCGGCC AAAGAGGCCT AACCGCGGNC GCTCTACAAC TAGTGGATCC CCCGGGCTGC	60
AGGAATTCGA TATCAAGCTT AATTAAGAAT TCGGCCAAAG AGGCCTAAGC GAGAAGAGTC	120
CCCGCTCCGT GCCCTACCAC TACTTTGAGA AGGGCCGGCT AGATGAGTGT CAGATGTACC	180
GTTTGCATGA GCAGGCTCCA AGGAGCGCCC ATCGCTTCAT TACCGAGAAC CCTGTGTTCT	240
CCCGCTGGGC CAAGAAGCGA CCCATCGTGT TCGCCCAACC GTCCTGGAGG GCCAAGTAGT	300
TCCTGTTGCC AGTGA CTGCC AGGCCTCAGC CAGGCCTGTG ACCCATTC CA GGCCAACACG	360
GCTCTAATGT GAGCATTTAT GACTCACCTT CTACCTGACA CCAGGTAGAA CATGAAGTCT	420
CTATTACCCA AACTGGGTA CACTCGGAGG TCGAG	455

## (2) INFORMATION FOR SEQ ID NO:547:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 401 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:547:

GAATTCGGCC TTCATGGCCT AGTCATTTTG TCAGCTTTCA CACAAGAATC TTTGATCCTA	60
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TTGTAATAGT TAATAAGGAA GTTCTTCTCT TGCTCAAAGA AGTCATCTAC CTCCTTAACT 120
CCAGTAAAAA GGACTTCATC AGCACTTTTC ACCACACTTT TGAAGAAGCC ACCAAACATT 180
TCTTTAGTAT TTTTCCGCCT AACACTTAGA TCCTGATCAT ATTCCAGGAA AACATGAAAG 240
TTGCGATCTT TACTGAGAAC AGGGTGAGAA GAAAGCCGCT GAAGAAAGAC TTCATGGGAG 300
GACACAGTCT TCTTAAACAC AGCGAGATAC TCAGCTTCCA GTTCTTGTTT CATCTGGGCT 360
TATTATTCCA CCTTCTCCA GTTCTGTCAT CTCTCTCGA G 401

```

## (2) INFORMATION FOR SEQ ID NO:548:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:

```

GAATTCGGCC TTCATGGCCT ACAAGCCCCT CTTACCTCTC TGGATGCTTT CTTTAACT 60
AACTCACCAC TGTGCTTCCC TGCAGACACC CAGAGCTCAG GACTGGGCAA GGCCAGGGA 120
TTCTACCCC TTCCCAGCT GGGAGGAGCT TGCCTGCCTG GCCACAGACA GTGTATCTTC 180
TAATTGGCTA AGTGGGCCTT GCCCAGAGTC CAGCTGTGTG GCTTTTATCA TGCATGACAA 240
ACCCCTGGCT TTCCTGCCAG ATGGTAGGAC ATGGACCTTG ACCTGGGAAA GCCATTACTC 300
TTGTGTCTGC TACTGCCCTC CCACAGTCAC CCCAATATTA CAAGCACTGC CCCATTGGCT 360
CGAG 364

```

## (2) INFORMATION FOR SEQ ID NO:549:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:549:

```

GAATTCGGCC AAAGAGGCCT ATGCTTTTCT TTGCAGCACT TAGCACAAAT AGTAATTTT 60
ATTTTACTTT TATAGATGTA TTTTATGTCC CTCCACCAGA CTGTATACTC CATGAGGACA 120
AGGATATTGA TGTTATGTT AACTCTTGTA CACTCAGTGC CTGGCACCAT GCCTGACCCA 180
GAAGAGGGAC TCGAG 195

```

## (2) INFORMATION FOR SEQ ID NO:550:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:

```

GAATTCGGCC AAAGAGGCCT AACATAATGC GCTAGCAGAC TTGGGAATTA GGGGAGAAT 60
GCTGCTCTAA ATTCAGGAAA TCATGGCACG GTTTCATATT GAACATGGTC TATTCCTACC 120
ACTAGCGCTT TCCTGGCTGA TTTCTTCTCC AGCTGGAGAC TTCTTTCTGG TTTTCCAAT 180

```

TATGCTCCAC CCTCACCCCA ACCCACCCAT AAACCACTGG CTGCCGGAAG CAGTATCTTT	240
CATAGTGGTG AGTTCTGGAT TTTCAGCAGT AATGGCCGAG AGTCAGGGAC CAGATGAGTG	300
TGTGTGAGCT GGTGAGAAAA GGTAGATTCC CTCGA	335

## (2) INFORMATION FOR SEQ ID NO:551:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 662 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:

GCCAAACATG TCTCACCNAA NNCCAAATGT CCCCNGGGGG AGCAAAATCT CCCCTGGACA	60
ACTGTGGAAT CACTGTNNGG AAGTGTTTAC TTGAGTGGTT TNCTGGCCTG GGCCTCATAC	120
TCTGAATTTT TGAAGTAAAT GGTCTGGGGG TGCTGGGGGT GGAGAGCAGA GCACTGGTAT	180
TTTAGGAGA TCCCCCTGTC ATTCTAAAGC ATATCCAGGG TTAAGCACCA TTAATCTGAN	240
GATCTNCNGT CTGATCTGCG GGCCCCCTTT CATCTANGTG CAGTATTTTT CTCTATGCTT	300
TTTAAAATAA TGAAAGTTTC TNGAACTCCA TCTGGACTTG AAATATAGCC TGCCACACAG	360
TTAGCAAATA TAGCAAGAAT AACAAAGTGT CTAAATGGAT TTTTAATTTA TTATGGCAAT	420
AGTACATTCC AANAGGGTGG CATTTTTTAA AATGAGATT TTCTTTTGGG CCTAAGATTA	480
CAGTCACATG GTTCCAAATT CAGAGGGTTC AAAAGGACAC AGAAAAGCCT GCTTCCCACT	540
TGNGCCCACT GGCCTCCCTT TTTTTCGCAT AAATGGCAGT ATATAGCTTT GTCTGTTCTT	600
TGTTNNNGA GCTTAATACC TTAGAGACAG ATTTNGTAT ATCTGTACCT ACAGAACTCG	660
AG	662

## (2) INFORMATION FOR SEQ ID NO:552:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 306 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:

GCTGTTTTAA AAGAGTTGGG GGAAGAGGTA GAAATGAATC TTTTGGTTTA GTTTTTTAAT	60
TCTCTAAGGA CAACATTGGG GAAGTGAGCT TTAGAGTTAT ATTTGCAGTA TTTATTTTAA	120
TCATGAAATA TTCAAGTCTA GGCCCTTGGT GAATTGAGGC CTGGTGAGTA TTTCTGCTTT	180
CCCCCTGGAG AGATTGAGAT GGTTCCTGAT TGGGAGCTTT AATTCTGTGG GCATTGTGG	240
GACTTACCAA AGAGGTATCT AGAGTTCCTT TAAAACCCCT GCCCTGTCCC TGCCACAAAA	300
CTCGAG	306

## (2) INFORMATION FOR SEQ ID NO:553:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 290 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:

GTCAAAAGAG	GAGCTAGGAC	CAGATCTCTA	AGTCTTACNG	TCCAGGTCAA	AAAACAAGTA	60
CTTTCCTATC	TGGTTATACA	GAAATCTGGA	AACAGTCACT	CCCAGCCTCA	CAATTAAAAA	120
AACCTGGACA	TACAGAAAGT	TCATAGTTTT	CCTTGAACTC	ATGATAGTGC	TGAGATTTCA	180
CGGCAACCAA	CTGGCCCAGA	TACTCCAGAG	TCAAAGACAC	TGTAAGGAGA	GTTGACATNT	240
GAGCATTAGA	CAAGACACAG	ATGGTANGAG	TTAAGCTAGG	GTTACTCGAG		290

## (2) INFORMATION FOR SEQ ID NO:554:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:

GAATTCGGCC	TTCATGGCCT	ACTCTATGGG	GATGAGGTAG	AGGAGAGCAA	GATATTTCGG	60
CAGCAGGGAA	AAGGGTAGAA	CAGAATAGGG	TGACACAATT	TACACTTGAT	ACTGCATTAA	120
CATCTGGTAG	AGTGTCTAGG	GCAAAGGTTA	GCCAAAATAT	AGCTGGATGG	TTGAGGGATT	180
TAGAAGGACT	TGGGATGAAT	CCATAGTCTC	AATGAATGGA	GAAAAAGTAA	CTCAGGAAAG	240
TAAATGCTGG	TGACTTATCA	GCGGGTGGCT	GGTGATGTTT	GGTTTGATT	GTGAAAGCTG	300
CTTAGACCAA	GATGGGCTGA	GGGAAGGGGA	GGAGAGTGAG	CATGTAGAGG	TTGAGGCACT	360
TGGTCTCGAG						370

## (2) INFORMATION FOR SEQ ID NO:555:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:555:

GAATTCGGCC	AAAGAGGCCT	AATTGCCAAT	CAACAACCTT	TCCTAATCCA	CCTTGATCCT	60
CAATCATAAT	ACTCAAAAAC	TGCCAAAAAC	AAAATCTTCC	TGACAAAAAT	ACAGGCCAAA	120
CTTCCTCATC	TGCTTTCCAG	GTCTTCTGTA	ATCTTATCCC	AGCTTATTTA	CAGTCTCTCA	180
TTTACTAAGA	AAACCCAAAA	TAATCTTTTC	CTGCCCCAAA	TTTATGTTCT	TCCCTTTTCT	240
TTTGTTTATA	CTACCATACA	TATCTAGAAA	TGATACTCAA	ATATTTCATC	TCAGCACCT	300
CGAG						304

## (2) INFORMATION FOR SEQ ID NO:556:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:556:

GAATTCGGCC	TTCATGGCCT	AGAGGGGAAA	GCATATCACT	AGGACTGTGA	CCCCTGTGCC	60
TACCCATCTT	ACTCTCTACC	TCTTAGGAAA	GTTTCACTGT	GTTTACTTGG	GACTTCTGGA	120

CTAGCTGCCG	TTTGCAACAG	TGGACTTACC	AGTTTGCCAC	TACTCTGCTA	CCTTTCTACT	180
GGTGACACA	CCTTAGTAAG	GCAGTTTGAT	TACTAAATGC	AGCTGTCTCC	AGAAATGGAA	240
TGATGCTATA	GGCCACTTAC	TAAATGAATG	ATCAGGAGTC	TCGAG		285

## (2) INFORMATION FOR SEQ ID NO:557:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:557:

GAATTCGGCC	TTCATGGCCT	AGCTGGATCT	GCCCACTGTG	CACTCCATCA	TCAGCAAAAT	60
GATCATTAAT	GAGGAGCTGA	TGGCCTCCCT	GGACCAGCCA	ACACAGACAG	TGGTGATGCA	120
CCGCACTGAG	CCCACTGCCC	AGCAGAACCT	GGCTCTGCAG	CTGGCCGAGA	AGCTGGGCAG	180
CCTGGTGGAG	AACAACGAAC	GGGTGTTTGA	CCACAAGCAG	GGCACCTACG	GGGGCTACTT	240
CCGAGACCAG	AAGGACGGCT	ACCGCAAAAA	CGAGGGCTAC	ATGCGCCGCG	GTGGCTACCG	300
CCAGCAGCAG	TCTCAGACGG	CCTACTGAGC	TCTCCACTCT	GTTTCCCGCC	TGGGCCATCC	360
AACCTTGAAG	TCCTAAACCA	CACCTCAGTC	ACTAAAGGTC	TGTCTCGAG		409

## (2) INFORMATION FOR SEQ ID NO:558:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:558:

GAATTCGGCC	TTCATGGCCT	AGGAAAAAGA	GATATAAAAA	AAAGAAAAAG	AGGNGGTACC	60
AGCCAACAGG	AAGACCACGG	GGAAGACCAG	AAGGAAGGAG	AAATCCTATA	TACTCACTAA	120
TAGATAAGAA	GAAACAATTT	AGAAGCAGAG	GATCTGGCTT	CCCATTTTTA	GAATCAGAGA	180
ATGAAAAAAA	CGCACCTTGG	AGAAAAATTT	TAACGTTTGA	GCAAGCTGTT	GCAAGAGGAT	240
TTTTTAACTA	TATTGAAAAA	CTGAAGTATG	AACACCACCG	TCTCGAG		287

## (2) INFORMATION FOR SEQ ID NO:559:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:

GAATTCGGCC	TTCATGGCCT	ACTTCTCAAA	AATAGATGTA	CTTGACTACT	CTTTTCTTGA	60
TTCTTCTGGG	AGTAACCATC	TCTTTGGAGA	TGTTTGTTAG	TAAGGTTATA	AAAATAACCT	120
TACTGAGGAA	CTCCCATGCA	ATCCTCTGAA	AATAATAAAA	ATTTCCTTAT	TTCAAGAACT	180
CTTATTTAAC	AAAGTAATTG	TAGGGTTGA	ATACTCTAGG	GGCAAATGAT	TTATTGTGCC	240
TTTTGTAAAA	GTCAACACTT	GGCAGGTGTG	TGTTTGACAC	TGGCTGATGC	TGGGCTTATT	300

TCTCTAAGAG TATGGTAATT CTAGTAAAGT AAAGAAAATT GTTTATCAGA TATTAGGAAC 360  
 TGTACATAGG CCCCCTCGAG 380

## (2) INFORMATION FOR SEQ ID NO:560:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 208 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:560:

GAATTCGGCC TTCATGGCCT AAAATTGTTC ACGAGGGATT ACGTGGTTTA CTGTCTGT 60  
 GTCCAGATAG CTTTATATTC TTTAAGATTC AGCTCGGATT CTTATCCTAT TTTTGCCATT 120  
 AACTTTCATT ATGATTTTGG CAAAGCCATT TTGTTTGCTT ACATTTTCA CTTTAAATGT 180  
 GGTGTCTGGC CTCCCCCA CACTCGAG 208

## (2) INFORMATION FOR SEQ ID NO:561:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 505 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:

GAATTCGGCC TTCATGGCCT ACAAACANTT TTTACTGNCT TATAAATAAA AACAGCGACA 60  
 CATCTAAAT GTGCACCTGT GCCGTGGCTG AGCCGCTGCA GTGAGGGCTA GTGTGCAACA 120  
 CCGATGCTGT GCTGGACGCG TGCCAGCCG GGTCCCTGA CAGGAGGCAN CCGGGGCCG 180  
 TCGTGTGTT TGCATGTTGC AGTCATGGG CCGGGNCGGC AGANGCCTGT GTGATNGTNG 240  
 CGTCCCTGGA AAAAGAAGNN GGNAGGCC CTCNCACNTG TANCCAGCC TGCAGANGGG 300  
 GNGTTNTGTG GGTCTTCCC CGTGATATG CGTGTGATNT CACCCATCCC GTGTGGGTGC 360  
 GCAGGAGGGG CCGAGGGAGG AGGGTGCTGG AGGGCGGAAG TTACCTCTGA CTGGAGGAGA 420  
 NACCCGGCCC GTGTNACCAG CANAGGTGTG NTCGTTCTAA AACTGGGAAA AATTGTCTCT 480  
 TAATTTTAAC CACAGTCCCC TCGAG 505

## (2) INFORMATION FOR SEQ ID NO:562:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 351 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:562:

GAATTCGGCC TTCATTAAAG AGATAAGTTA GAAAAGTCAA AGCGAGAACG GCATAACGAG 60  
 ATGGAGGAGG CAGTAGGTAC AATAAAGAT AAATACGAAC GAGAAAGAGC GATGCTGTTT 120  
 GATGAAAACA AGAAGCTAAC TGCTGAAAAT GAAAAGCTCT GTTCCTTTGT GGATAAACTC 180  
 ACAGCTCAAA ATAGACAGCT GGAGGATGAG CTGCAGGATC TGGCAGCCAA GAAGGAGTCA 240  
 GTGCCCCACT GGAAGCTCA GATTGCGGAA ATCATTCAGT GGGTCAGTGA CGAGAAAGAT 300



CCCCGGGGTT ACCTTCAAGC TCTTGCTTCC NAGATGACCG AAGAGCTCGA G

351

(2) INFORMATION FOR SEQ ID NO:563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:563:

GAATTCGGCC TTCATGGCCT AAAAACTGT CCATGGCATG AAAGACTTGG ACCGCCATCT	60
CAGAATCCAC ACGGGAGACA AACCGCACAA GTGTGAGTTC TGTGACAAGT GCTTCAGCCG	120
GAAGGACAAC CTGACCATGC ACATGCGGTG CCACACCACT GTGAAGCCAC ACAAGTGTCA	180
CCTGTGTGAC TACGCTGCCG TGGACAGCAG TAGCCTCAAG AAGCACCTGC GGATCCACTC	240
TGATGAGCGG CCGTACAAAT GCCAGCTCTG CCCCTATGCC AGCCGCAACT CCAGCCAGCT	300
CACCGTCCAC CTGCGATCTC ACACGGGTGA GTCCTTGACC AGGGGTCTCT GAG	353

(2) INFORMATION FOR SEQ ID NO:564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:564:

GAATTCGGCC TTCATGGCCT ATAGAATTCC TAGACTTTAC AGACTAATAG TTTGACATCT	60
ATCTCTGGCA AAATTCGAAA CTTAAACATT AAACAAGGGA AAATGAGGGG TGGAGGNAAA	120
GACTGCGGAT TTCTAGGAAC TAACAATTG CTAAGNATCA TTCATTTTAA AACTAATGTT	180
ATTTACTTTT GTGGTAGATC AGGGNATATG CAAGATCTTT ACTTTTCAGC AAGACATTTT	240
TCTCATAATG TCCTTATGGA GAAGACTGCT CTATGGACTA GNATAGTTTG ATAAGAAAGG	300
GCTGAGTCCA GCGNATTCAT TAGTTCAAGC AAAATCTACT GGAGGCCAAC TAGATTTCCA	360
GCCATTATCG TACTTGGCAC TTTCNATACT TTGAATTTTA ACCACCACAC CTCGAG	416

(2) INFORMATION FOR SEQ ID NO:565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:565:

GAATTCGCCC TTCATGGCCT AAGACGGGGT TTCACCATGT TAGCCAGGAT GGTCTCGATC	60
TCCTGACCTC GTGATCCTCC CGCCTCAGCC TTCCGAAGTG CTGGGATTAC AGGCGTGAAC	120
CACCACGCCC AGCCATATAT CAGGAAGTTG AGCATCCATG GAGTTTGGTG TCCAAGGGAG	180
GTCCTGGAAC CAATCCGCCA TGGATACTGA GGGATGACTA TAATATGAAC CTTGTATGTA	240
TGTAATTTAC CATTTTCTAG TTAGCCACAT TAAAAAAGGA AAAAGAAACA GGTGAAAAAT	300
ATTTAAAAAA TACGTTAACA CAATATATCC AGAACATGAT TTCACATTGA AATCAATATA	360

AAAATTACTG AAATAGTTTA CAGTCTGGTG TGCATTTTAG ACTTAAAGCA TATCCCTTTG 420  
GGCATGGTGG CCCATGCCCTG TAGTCCTAGC CACTGAAGGC TCGAG 465

## (2) INFORMATION FOR SEQ ID NO:566:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 357 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:566:

GAATTCGGCC TTCATGGCCT ACAGCGAGAA GGAGTGTATG AGTGTGAGTG TGTGTGCATG 60  
GAAGTTGGGC ACTGGGCGTC TGANTCCTTC CCCACCCAAG AGAGGAAGGA CCCCTCACCA 120  
CCCCCACTGG CGAGACAGTT TACTTTGCCG ACTTGCCATG TTTTGGCCAA AACCAAGATT 180  
TTGAAGGAAA TGAGTGGCCA GCGCCAGGGC CCAGGCCATG TGGCCTGCCC AGCCTCAATG 240  
TNACTTGGTG GCGGGGTGGG GTGGGGGTGG GCAGCAGCAT CCCAGCCTTG AGATGCTTCA 300  
CTTTCCTTCT CTGTAACCAG ACTTTGAAAA ATTGTTCTGT TCATCAGGCA TCTCGAG 357

## (2) INFORMATION FOR SEQ ID NO:567:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 336 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:567:

GAATTCGGCC TTCATGGCCT ATCTGCACTG AATTAGAACA AAATTTAGGA GACTTCTAAT 60  
TTGAAGCCAG AGGTGCTGAC TTTTGAGTCT TTGGAGATTG CCTGTTGGAA ATATTCCTGT 120  
TGAGGGCCAA TGTCCCAATG GGCTCTGAAG ATGAGAAGGA TCCCTGCCCT ATGTGGATGC 180  
CACTGGATCT GGAATCATTT CTGTGGCTCA GATTTCTGTA CACATTCTGC CAGGACAGGA 240  
GCAGCCGTAT TGGGAAAAGA AGGGGGACAA TAACTAGAAA CGAACTAAGA TGTGGCCCTT 300  
GCTTTTGATAC TTTTAATTTA ATGGGAAACA CTCGAG 336

## (2) INFORMATION FOR SEQ ID NO:568:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 481 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:568:

GAATTCGGCC TTCATGGNCT ACCTGGACCT TGGGTGGCAG GCCTGGGGCC TTCAGTCTCT 60  
AATTCAGGAG GTAGCCAGTC GCTGGAACTA AGANTGAAGT TCAGTGTGTG TTGCCATAGC 120  
TGGAGGGAAG AGGGAAAGGA GCGCTGCAGG GGAGCAGAGA CCTCACCTT CCTCTGCCGA 180  
CATCAGGCTG CCGGTGCTGG ACGGGGCCCT GGCAACCGTG GCAGGAGTGG TGATGTCCGA 240  
TGATGGTAAC AAGGGCTTCC TGAGGACCCC GAGCTGTCTT AAGGGCTCTT TACCTGGAGT 300  
AAGTATCCCC TTTAATCCTC CCAACAACAC TGTGAAATTG ATTCTGTTGT TATTCCTATT 360

TCACCGATGA GGAACCCACA GCCCAGAGAT GTTAAGTAAC CTGCCCAAGC CTCCCTCTGA	420
GCGATGGCAGA GGGAGGGTCC GAATGCGGAA AGTCTGGCTT CAGTGCCCCC ATCCTCTCGA	480
G	481

## (2) INFORMATION FOR SEQ ID NO:569:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 472 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569:

GAATTCGGCC TTCATGGCCT ACTCATCATT TGGAAAATAC TTGATGGCAG GAGAACTTGC	60
TTAAACTAA AGGTGGAGAA AGAGTAACT TCCAGGACAA CCCATTATAG CTCACTTCTT	120
ACCAACAAAG CAGTTTTTAT ACAGCACCTT AGGACTCATT TCTAATGTCA ACCCAGATGG	180
CCAGTAAAGG CAAGGGAAGA GGCTAAGTGA CTCACAAAAA TCTCTGATAT TGAGGTCTAA	240
TGTGAAGGCT ATAGATAGGA ATTCCCCACA AACTTCTAAT GAGGACTAAT ATGAACAGCA	300
AATTGGAGAA GACACCAAGG ACCTAATTTT AGTTTCTACTA GCCGTGGGAC CTTAGAAAAA	360
AGACCATTG CTCTGGACTT TTGTTTCCCA AGCCATAAAA TGTGGAAGAA TCTTCACAAT	420
TTCAAGTTG TCATGTATAT TTCCCTTTA CAGAGAAAGC TGAAGCCTCG AG	472

## (2) INFORMATION FOR SEQ ID NO:570:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 487 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:570:

GAATTCGGCC TTCATGGCCT AGAAAGGATC AAGCTGATCA GAAGCGGGAG CTGCATTGAG	60
GGAAAAATAT GGCCAGAGAA GGCCTCACTG AGGAGGTGAC GTTGGTGATG CTGGAGCTCA	120
GATCTGAAGG GGAAGAAGGA AGCAGCCACA TATAGAAGTG AGGGAGGGGG CTTAGGCAAA	180
AGGAACAGCA AGCGGAGAGG CCCTGAGAAA GGAAAGGCTT GGCTCGCTCA CCTGCAAGGG	240
CCCCCTGGCT TGACATAGTG AGAAAGGTGT GAAGATGAAT TTGGAGAAAG GCAGGGACAG	300
ACCACAGGAG ACCTTAGATT TGATTCTGAG GGCGATGGGA TCCCTTGAGA GGATGCTGAG	360
CAGGGGAGAG ATGTGATCTC CTTTTTATTC TAACATGATC GCTGCAGCTG CTGCTGGAGA	420
ATGTTGTCAG GAGCGAGAGT AGAGACTGGG AAGTCTGTG CATCCTCTAA GCNACAGGCG	480
TCTCGAG	487

## (2) INFORMATION FOR SEQ ID NO:571:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 456 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:571:

```

GAATTCGGCC TTCATGGCCT AGAATAAATT GTGATACAAA AAAAAAAAAA AAAAAAGAGT      60
GTACACTATG AATGGGTTGG TCGTTTTCTT CCTGGCTTTT TTTCTTTTTC TTCAGAGTTA      120
GGAAATACTT TTATTTTTC AAGGAAAATT CATCATAAAT TTGCGCTGGT ACTTTTGGAC      180
ACAGGATTCT TTCAGTGAAG CTTTGCCGGC CGGAAATCTC CATGGCCGGC CTGCCTCTG      240
CCCGGTCTTC ACTGAAGCCT GCTGGGCTCT CTCCACCTAC TTGGTCCATC AGTCTGTGCT      300
TGGCTCATCC TAGCAACCTG GATCCCGCAC CCGTATGGC ACCGTGCTTG GCTGGAGGCT      360
GGTCCGAGCG TCCGTGACTA GCTTCCACCT TCGGCGCCAG CTTTGTGACA AGGGGAACGC      420
AGTGGCACCC AAAAATCTCG AGACATGAGA CTCGAG                                456

```

## (2) INFORMATION FOR SEQ ID NO:572:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:572:

```

GAATTCTAGA CCTGCCTCGA GATGCCCCGAC TACTACAAAC CTCAGTACCT GCTGGACTTT      60
GAAGACCGCC TTCCCAGCTC GGTCCACGGC TCAGACAGTC TGTCCCTCAA CTCTTTCAAC      120
TCCGTCACTT CCACCAACCT GGAGTGGGAT GACAGTGCAG TTGCCCCATC TAGTGAGGAT      180
GGAGACCTCA CAGACACGGT CAGTGGTCCC CGCTCCACAG CCTCCGACCT GACCAGCAGC      240
AAGGCCTCCA CCAGGAGCCC CACCCAGCGC CAGAACCCCT TCAACGAGGA GCCGGCAGAG      300
ACTGTCTCCT CCTCTGACAC CACCCCGTGT CACACCACCT CTCAGGAGAA GGAGGAGGCC      360
CAGGCCCTGG ACCCGCCGGA TGCCTGCACG GAGCTCGAG                                399

```

## (2) INFORMATION FOR SEQ ID NO:573:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:

```

GAATTCGGCC TTCATGGCCT AGATTGGGT TAGTGGTTTT CTTTAGCAT GTTGAAAATG      60
TCACCCAACT GTTTCTGGG TTCCTTTGAA AAGCCAGCTG TCTGTCTGTC TGGTTGTCAT      120
GTCTGAAGGT GATGTGTCTT TACCTCTGGC TGCTTTAAGT ATCTTTTGCC TTTTCCCCT      180
TTGTGAATGT TTTTGCTGAA GTGTAACATA TACACAAAAG AGTGTGCAA TCATCAATGC      240
TTGATGGATT CTCGAG                                256

```

## (2) INFORMATION FOR SEQ ID NO:574:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:

GAATTCGGCT TCATGGCCTA GAATCATGCA TTTCTTTTC TTTTTTTTTT TCCCGTTGGC	60
TTTGTCTATG CTGGTGGCAT CCAGGGCATT GCTTGTCTC CCTGATTATG CCCAGGATTC	120
AAGGTCTTCT TATTTGTGGG GAGGCAGGCT GCCCACTGGG ACGGTTTTTA GTGTGTTTNC	180
CATTCCTGGC TCCCTCGAG	199

## (2) INFORMATION FOR SEQ ID NO:575:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:575:

GAATTCGGCC TTCATGJCCT AGGATTTGAA GAAGTTGGGA AAGCATTATG TAGATTAATA	60
TACTGTTGG TTCCTATCT ATGTGGAAGG TCATATTAGC TGCAATTATT TAATTTGCTG	120
TGTTATTTTG TGTTATATAA CACAAATATA TTTGTATATT AACTTCATT TTAGTGTCAT	180
TTTTCCTGTT GTATACAAA TGAACATC TTGTAATTAT TTTCAAATAT AGAAGTATAT	240
ACATTAGATG GATTTCCAAG ATTTGTAAAG NAAATCTTAA ATCAGTGTT TGAGTTATTT	300
AATTTTAAA TTAATCTACA AATTATGCAC NACAACTAG CAACTCGAG	349

## (2) INFORMATION FOR SEQ ID NO:576:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:576:

GAATTCGGCC TTCATGGCCT ACAAATTTTG CTCACTTTCA TTAATCAGTT GCTCAGATAG	60
AAGGAAATGA CATCTGGTTC TGTCTTCTTC TACATCTTAA TTTTGGAAA ATATTTTCT	120
CATGGGGTGG ACAGGATGTC AAGTGCTCCC TTGGCTATTT CCCCTGTGGG AACATCACAA	180
AGTGCTTGCC TCAGCTCCTG CACTGTAACG GTGTGGACGA CTGCGGGAAT CAGGCCGATG	240
AGGACAACTG TGGAGACAAC AATGGATGGT CTCTGCAATT TGACAAATAT TTTGCCAGTT	300
ACTACAAAAT GACTTCCCAA TATCCTTTTG AGGCAGAAAC ACCTGAATGT TTGGTCGGTT	360
CTGTGCCAGT GCAATGTCTT TGCCAAGGTC TGGAGCTTGA CTGTGATGAA ACCAATTAC	420
GAGCTGTTCC ATCGGTTTCT TCAAATGTGA CTGCAATGTC ACTTCAGTGG AACTTAATAA	480
GAAAGCCCCT CGAG	494

## (2) INFORMATION FOR SEQ ID NO:577:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:

GAATTCGGCC TTCATGGCCT AGGCACGTTA AATTTAAAA GTTANAAAAA GAAAGATGCT	60
--	----

TTTTGCAGCA GTTCCAGGGT AAACGGCCCC ATGCAACACA AACCTCCGGG AAGGGCATT	120
CAGCCTTGCA GTGGGCCACG GAGTGCACCA CGCGGCGCTC AGCCCCCAG GGAAGCGATG	180
CCCCACATCG GGCCAGAAAC AAAAGGGGGT GAGATAAAGC ATGCTCGAG	229

## (2) INFORMATION FOR SEQ ID NO:578:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:578:

GAATTCGGCC TTCATGGCCT AAGGAGTTTG AGATATATTT AGGAAGCAGA GCCTATAAGA	60
CATGCTGATC ACTTGCATAC ATAACTGAG AGAACTAGAG GTATAGAAGA CTTCTAGAAC	120
TTGGAGAAAT TGGATGAATG GATGTATTGT TATTGATGTA ATGAACCTTA GAGGTGGGTG	180
GGATCAGAAA GATCTATTTG CTTTCAAAGG AAATGGGGAG TGGACAGGTA TGTGGCAGC	240
ATAAGAACTG GAATAACAGC ACATCTCATT CATGCCCTAA AAGAACGTGA AACTTTGAAT	300
GTACAGCAAT GGTATTCAT AGGTATGACT TTGCCCTTAA AGGACATAGA CACCAGGGAT	360
GTTGCTAAAT ATCCTCCAAT GCACAACACA ACCCTCGAG	400

## (2) INFORMATION FOR SEQ ID NO:579:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:

GAATTCGGCC TTCATGGCCT ACGAGGACGA GGACGTCAAG GATAACTGGG ATGACGATGA	60
TGATGAAAAA AAAGAGGAAG CAGAAGTAA ACCAGAGGTA AAAATTTTCA AAAAGAAAAA	120
AATAGCAGAG AAGATAAAG AGAAAGAACG GCAACAGAAG AAAAGGCAAG AAGAAATTAA	180
AAAGAGGTTA GAAGAACCCG AAGAACCTAA AGTGCTAACA CCAGAAGAAC AATTAGCAGA	240
TAACTGCGG CTAAGAAAT TACAGGAAGA GTCAGACCTC GAATTAGCAA AGGAACTTT	300
TGGTGTTAAT CTCGAG	316

## (2) INFORMATION FOR SEQ ID NO:580:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:580:

GAATTCGGCC TTCATGGCCT AAGCGAGGCC TGAGCCTCTG CGTCTAGGAT CAAAATGGTT	60
TCAATCCCG AATACTATGA AGGCAAGAAC GTCCTCCTCA CAGGAGCTAC CGGTTTTCTA	120
GGGAAGGTGC TTCTGAAAA GTTGCTGAGG TCTTGCTCTA AGGTGAATTC AGTATATGTT	180
TTGGTGAGGC AGAAAGCTGG ACAGACACCA CAAGAGCGAG TGGAAGAAGT CCTAGTGGC	240

AAGCTTTTGTG ACAGATTGAG AGATGAAAAT CCAGATTTTA GAGAGNAAAT TATAGCAATC 300  
 AACAGCGAAC TCACCCAGAC TCGAG 325

(2) INFORMATION FOR SEQ ID NO:581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:581:

GAATTCGNCC TTCATGNCCT ANGAGAAGNA CCCAGACCCC CCCAAGAAGG AGGAGGANCN 60  
 CCNNNGAGNC NCTNCTCCAG NCGGANGAGG AGCGCAAGGC CAAGTNCGCC AAGATNGAGG 120  
 CGGAGCNCGA GGCNTGNNC CAGGGCATCC GAGACAAGTA CGGCATCAAG AAGAAGGAGG 180  
 AGCGCGAGGC CGAGACCCAG ACGCCGCCAA GAAGGAGGAG GAGCGGCAGG AGGCGCTGCG 240  
 CCAGGCGGAG GAGGAGCGCA AGGCCAAGTA CGCCAAGATG GAGGCGGAGC GCGAGGCCGT 300  
 GCGCCAGGGC ATCCGAGACA AGTACGGCAT CAAGAAGAAG AAGAACGCTC GAG 353

(2) INFORMATION FOR SEQ ID NO:582:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:582:

GARWYKCSS YYTTNANGGC TAGTCACTGG CAGGGCCACC CAGAAGCCCC GCAGATGACG 60  
 GAGCTGAGAA CAGGGAATTN ACCTNCACGT GTTGCCATT CTCTANTGGA AAGTCCTTGG 120  
 GAGGTGGCTG GGCTCAGCCT GAGCTCAGGG CTTTTCGGTG GGGTTGGGGC AGGGGCAGGG 180  
 CGGGCNNTTG CAGGTGGCAC AGGCTTCATC AAGGCAGGAC ACGGGNTTCA TCAAGGCAGG 240  
 AGCCACAGCG CCCGAGCCCT GGCAGGGGAG GTAAGGCCCA GGATGGGGCA GGGCCGTGTG 300  
 CTCCTGGNAC GGACATCCTT NTCTGCCAGA GACCTGCTCC CCAAGCCCTG TCCCTCCCAA 360  
 TCCCCAGGCA GCCCACTCTG CCCTCCATAG ATGAATCTAA TATTGAATTT CTAGACCTGC 420  
 CTCGAG 426

(2) INFORMATION FOR SEQ ID NO:583:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:583:

GAATTCGGCC TTCATGGCCT AAGAAAAGAA AGTAAGATTA TCTCCAGCCA AAATGTCAAC 60  
 CAAGAATTCT ACAGATCTAG TTGAATATGT TGACAAGAGT CATGCTTTTC TCCCCATCAT 120  
 TCCAAACACC CAGAGAGGTC AGCTAGAAGA CAGACTGAAC AACCAGGCAC GTACCATAGC 180  
 TTTCTTCTT GAACAAGCCT TCCGCATCAA GGAGGACATC TCTGCTTGCC TGCAGGGGAC 240

CCATGGCTTT CGAAAAGAGG AATCGCTCGC CAGGAAGTTA CTGGAAGGCC ACATCCAGAC	300
CATCACCAGC ATCGTCAAAA AACTCAGCCA AAATATTGAG ATTTTAGAAG ACCAAATAAG	360
AGCTCGAG	368

## (2) INFORMATION FOR SEQ ID NO:584:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:

GGAATTCGGC CAAAGAGGCC TAAACGACTC TTGCCCCTGT TTCTTCTTGG CTTCCTTGC	60
GTAACAAGGA TGAAGGAGGT GGTTTAACTT TATTTTGTGC CTTTAACTTT TTAAAGTCTA	120
AAGTAAGTGC TTGAATCGGG TGGGTTTCA TTTTTTGTCT TTCTCACCCC TCAGGTGGC	180
CCCTAACTTG GCCTCTCACC CTCGTGTCAG CTGTTAGACA CTGACTCAGT GGCTCAGAAT	240
ATGAAAGGCT CAGGAAGTAG CATGCTGGCC CCACCTCCCT GTCCCCATAC CTTAGCAGAG	300
CAGCTGCCCA GCAGGGCCTC CTTCTCTTTC CTAAGAGTTT ACTCCATCCA TGGTGGGTGT	360
CTTGGTAGGC CCGAGATACG AGAGGGAGTG CTGCTGTTAC AAGAATTAC AGTTGTTCTC	420
TTCGGCACAA GCTCGAG	437

## (2) INFORMATION FOR SEQ ID NO:585:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 565 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:585:

GAATTCGGCC AAAGAGGCCT AGTGCAGAGT TGCAAGCAAG TTTATCAGAG ATACGCCATG	60
AAGTTCGTCC CCTGCCTCCT GCTGGTGACC TTGTCCTGCC TGGGGACTTT GGGTCAGGCC	120
CCGAGGCAAA AGCAAGGAAG CACTGGGGAG GAATTCCATT TCCAGACTGG AGGGAGAGAT	180
TCCTGCNCTA TCGTCCCAG CAGCTTGGGG CAAGGTGCTG GAGAAGTCTG GCTTCGCGTC	240
GACTGCCGCA ACACAGACCA GACCTACTGG TGTGAGTACA GGGGGCAGCC CAGCAATGTG	300
CCAGGCTTTT GCTGCTGACC CCAAACCTTA CTGGAATCAA GCCCTGCAGG AGCTGAGGCC	360
CNTTCACCAT GCGTGCCAGG GGGCCCCGGT GCTTAGGCCA TCCGTGTGCA GGGAGGCTGG	420
ACCCAGGCC CATATGCAGC AGGTGACTTC CAGCCTCAAG GGCAGCCCAG AGCCCAACCA	480
GCAGCCTGAG GCTGGGACGC CATCTCTGAG GCCCAAGGCC ACAGTGAAAC TCACAGAAGC	540
AACACAGCTG GGAAGGAATC TCGAG	565

## (2) INFORMATION FOR SEQ ID NO:586:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:586:



GAATTCGGCC AAAGGGCCTA CAGAATAGCG GTACCATGAT AGAATACTGC AATTGTGGTC	60
AGAATTACAG TATGCACAAA GAATTAATTA GCATTATTAA AGAGTCCTCA CTAAACATTT	120
CATATGATCA CACTGAAGAA CTGTAACATT CCATAGAGTG AAGTGGTTCA AATTTCTCTT	180
GGAATTTTTA CTTTGTGG CCTTATTTTA TGATCCTTTT CATATTTCTT TTGACTTAGA	240
GTATTAATAC ATGGCCAAAA TAATTTAGTT ACTACCTCAT ACAAACAATA TAATGGTTAC	300
TCGAG	305

## (2) INFORMATION FOR SEQ ID NO:587:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:587:

GAATTCGGCC AAAGAGGCCT AGTTGTTTTT AATGGCACAG GACTCTTCCA CTTTGTGGTC	60
CTCCTCTAGC ACAATACTGG ATGGCTGGGG CAAAAGATTA AAGGAAGTCT TTTCCACATC	120
ATTTTCTGCG TGTTCTCAA ATCTTTTAC TAAATTGAT ACAAATTCCT CTATTCTTG	180
ATGATATTGC TTGAAATAG CATTGTTTAT GAATAGAATC TGTAATATAG GTCCATCTAA	240
CTTAGTATCG TTCACCAATA TTCCACTCGG TCGAGTCAGA ATGTTCAATT TTCGTTAAG	300
TTCTTGATTG TCGGCGCGGA GCTGCTCGAT GGTCTCCACG CACTCGAG	348

## (2) INFORMATION FOR SEQ ID NO:588:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

GAATTCGGCC AAAGAGGCCT ACTCATGACA GGATGACAGT CACATTGGT AGACACCATC	60
AACCAATGAT CTCTAATTTG CGGCCCCCAA CAAGCAATGG GGTCTGTGG GCTACATCTG	120
GAATTTGAAA TGTCTCATGG AAATCATGTT CTTACCTGG AGAAGGGTGG CTGCTTAGGT	180
GCTACTTAGG AAACCAGTCT GGCAGACCAG ATCTTCCCA ACTCAGGGGC TATGCGGGGA	240
GAAGTATTAG GAGCCCCTGA GCAGGAAGGA TGTACTTAGG AAGGCTACCG GGGATGGGGA	300
AGGGTAAAAG AGCTTAGAAG CCTGGGTGAA GTTTGGGTAG ACCAAAAACA GGAGGGAGGG	360
AGGGAGGATG TTCCCTTGA ATACAACTA GAGAAAAGCT TAGGGGANCA AGTCTTTTAA	420
TTTGGGGACA GTGAAGAGTT TCCTAAAAAT TCCTGGCCC CCAGGCCTTG GCTAAAAACC	480
CTCGAG	486

## (2) INFORMATION FOR SEQ ID NO:589:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:

GAATTCGGCC AAAGAGGCCT AATTGATTGT GATTAACCA	GATGTATGGA AAACAGTTTT	60
AAGTGTGTAG TGCATGTATC TCATAAGGTC CATTAGACG	TTCATTATTT TTCAATTGAT	120
GCGTCTTAAG CCCCACTTGA TGTGTGTTGT AGTGCATTC	CACAGAAGGA TTCTGCACTG	180
TGGGATTGAG TTCATTTTGT TAATTGCATA ATACAACCC	ATCGTGTTTC ATAGAAAATA	240
GTAAATACTC TTGCTTTTAT TCATTGGTAT TCTTTGATAT	TACTGAAGAA ATACCAAAGA	300
AGCAAAGGAG CAAAGAAATA CCAAAGAAGC AAAGGAGCAA	GTGAATAGTT CTTCAAACCT	360
TTACATATTA AGGGCACGAA TGTTCCTTGA AATGTGGACA	CATACTCGAG	410

## (2) INFORMATION FOR SEQ ID NO:590:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:590:

GAATTCGGCC AAAGAGGCCT ACGGCCAAAG AGGCCTAATT	GAATTCTAGA CCTGCCTCGA	60
G		61

## (2) INFORMATION FOR SEQ ID NO:591:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:591:

GAATTCGGCC TTCATGGCCT ATCTAGACCC AAATATTTTG	AATATGTTAT CTGTCTCTTT	60
TTCTTTTGT TATATAGAGA GATTGATGCA TAAAATCTGT	GTTGTATGA CTGTAATTCC	120
AAGTTTAGCG AAATTGTCCC TAGGACAACA CACCAACGGC	CATGAGCTGT CTCGGTCTCG	180
CAAGCTTAGT CTCCGATCCT GCCCACTCGA G		211

## (2) INFORMATION FOR SEQ ID NO:592:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:592:

GAATTCGGCC TTCATGCCTA GCCGGACCTG GTGCTCCTTT	CCTTGGTGCT GGGCTTCGTG	60
GAGCATTTTC TGGCTGTCAA CCGCGTCATC CCTACCAACG	TTCCCGAGCT CACCTTCCAG	120
CCCAGCCCCG CCCCCGACCC GCCTGGCGGC CTCACCTACT	TTCCCGTGGC CGACCTGTCT	180
ATCATCGCCG CCCTCTATGC CCGCTTCACC GCCCAGATCC	GAGGCGCCGT CGACCTGTCC	240
CTCTATCCTC GAG		253

## (2) INFORMATION FOR SEQ ID NO:593:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 190 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:

```
GAATTCGGCC TTCATGGCCT AAAGAAATGA AATAATATCT CTGAATTTTA GTCCATGTTT    60
TCAATGATTT CTGACTTTAT TATATTAAC TTTATTAATG ATCACAATTT ATTTTGTAAG    120
TTTTGCAGCC AAAGGGACAA TTTATTTTGT AAATTTGGGA TTCTATTTGC AAAATAGGGA    180
TCGACTCGAG                                         190
```

(2) INFORMATION FOR SEQ ID NO:594:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 208 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:

```
GAATTCGGCN TTCATGGCCT ACGGGGAACA GAGGATGGCG GAGGAGGGAA CACACAAGCA    60
GGAGCCCATG CAGCTGGGAG CCACTGAGAT CCCAGCTGGA GGAAGAGTGC CCTGGCACTG    120
AGGTCTAATG GCTGTCCAGC TGCTGCCCCA GGATGTGAGG GCAGGTGGTA GGCCATGAAG    180
GCCGATTGAA TTCTAGACCT GCCTCGAG                                         208
```

(2) INFORMATION FOR SEQ ID NO:595:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 120 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595:

```
GAGCTATAAA ACAGAAATAC ATGCATAGCT GCAGAAACCA TGATAGGTAG AGGACTTTTC    60
TTTTGGTTTT GTTTGTTTT GTTTGTTTT GTTTTGGTT TTACAGAGAA GAGACTCGAG    120
```

(2) INFORMATION FOR SEQ ID NO:596:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 282 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596:

GAATTCGGCC TTCATGGCCT AAGAAACCAA ATTAGCAGAC GGATAGAATA TAAAGCANGA	60
GGCAATACTT ATAGTGTATT AAGAACTTG CTAGACCCCA TCCAAATTAC TCAGTCTACT	120
GTTGGTTGAT AGAATTACTT TAGGAAGAGT ACGTTTTTCC TTGGAAATAC ACTGGAAGTG	180
GTACCAAACA AATCTAATAA AATGATGTTA AAGAGATTG CAGTAATTTT TATCNACTTT	240
CAGTTTGCAA ACTTTTATAA AGATATGAAA NGGACACTCG AG	282

## (2) INFORMATION FOR SEQ ID NO:597:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:

GGCCTTCATG GCCTAGACAC ATACAAAGAT AAGGCTTTGA TAAAATTCAA GAGTTATTTG	60
TATTTTGAGG AAAAAGACTT TGTGGATAAA GCAGAGAAGA GCCTGAAGCA GACTCCCAT	120
AGTGAGATAA TATTTTATAA AAATGGTGTC AATCAAGGTG TGGCTTACAA AGACATTCT	180
CGAG	184

## (2) INFORMATION FOR SEQ ID NO:598:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:

GAATTCGGCC TTCATGGCCT ACTTTGAGTT AAATAGAGAG TTGATTAAAT GCATATATTG	60
ACAGTTACTG ACTCAGTAAG CTTCATAATT CTAGGAATCA ATCACTGCTG ATTCATATGT	120
TTAGATATAT TCATTTCTGT CTTTCTGTTT CTTAGGCCAA AAAGAAAAAA GAAAACCAAT	180
ATTTAAGAGA AGAGAAAAAT GAAGACGGGA CATTTTGAAA TAGTCACCAT GCTGCTGGCA	240
ACCATGATTC TAGTGGACAT TTCCAGGTG AAGGCTGAAG TGTTAGACAT GGCAGATAAT	300
GCATTTGATG ATGAATACCT GAAATGTACG GACAGGATGG AAATTAAATA CGTCCCCCA	360
ATCCCTCGAG	370

## (2) INFORMATION FOR SEQ ID NO:599:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:

GAATTCGGCC TTCATGGCCT AAGACTCTTA GATCTAAAAG GAAACTGACT TGCCACCTTG	60
CCAGAGGAAT TCTTGAAATG TTTCTGCAGC CACTTGGCCT TGAAAATAAA GGGTGCAACT	120
CTCAATCTT GTTCTAACCC GGCTGGAGGA ACCACAAGAC CCAATGAAAT AGCATTTTCT	180
CTCCTTTTCC CAGCACTAGT ATATAACCTA TGAGGAACCC TTGTCTCTGA ATCTGCTCAG	240

```

CTTGAAATTT TGTCTCTGAA GGAAGAGAAT GATCTCAGCC CTAGTCTGAC AGTCCTAGAT   300
TTCTGTGAAA TAAGAGTATT CTTCAACTTA GTGCTCACAC TCACATACCA TGAGGGTTCT   360
CTGCAGAGGA CTCGAG                                     376

```

## (2) INFORMATION FOR SEQ ID NO:600:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:

```

GAATTCGGCC TTCATGGCCT AAGTCACTAT TTGGTAGCTG ACTTTGTGCC CTGATTAGAA   60
ACGTGGCTCC TTTTC.TGGT AGTTGTTCTT AGAACCTATC AACCTGCAGA GATTTTTATT   120
TTCATGGAAG GGAAGTGAAG GTTCTTTCTT TTGCTTCAGA CGGTCAATC TTTAGATCCT   180
GAAGGGAGAG ATGCAGCTTG CTCTCTCCAG AGTCCAAATG CAGCAACAGA TTTTGCCTCC   240
ANGCAAGCAA GATATGCTAT AAAAACCTGC NACATTCCCT CACCAGCTCC TCTCTTTGAA   300
TTTTCGATGC CTCGATGGTC ATTTGAGATG GACAGCTTGT AGTGAGATAG CTGTGGCATT   360
GGAAGGGGGG AAGCATGCAC CATTTTCCCT AGGCCTTCC TGCTTTTGCT TGATAAGCAA   420
TTCTTTGAAT GGCATGTTCT CCACCTCTAG CCACCTTGTG TGTAGTCCCT ACTCTCGAG   479

```

## (2) INFORMATION FOR SEQ ID NO:601:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:601:

```

GAATTCGGCT TCATGGCCTA CACAGGCATA ACAGTCAGTC GGGAAAAGGT CACTGAAGTT   60
GCCCTTAAAG GTGAAGGGAC AGAAGAAGCT GAATGTAAAA AGGATGATGC TCTTGAAGT   120
CAGAGTCACG CTAAGTCTCC TCCATCCCCC GTGGAGAGAG AGATGGTAGT TCAAGTCGAA   180
AGGGAGAAAA CAGAAGCAGA GCCAACCCAT GTGAATGAAG AGAAGCTTGA GCACGAAACA   240
GCTGTTACCG NATCTGAAGA GGTCAAGTAAG CAGTCCTCC AGACAGTGAA TGTGCCATC   300
ATAGATGGGG CAAAGGAAGT CAGCAGTTTG GAAGGAAGCC CTCCTCCCTG CCTAGGTCAA   360
GAGGAGGCAG TATGCACCAA AATTCAAGTT CAGAGCTCTG AGGCATCATT CACTCTAACA   420
GCGGCTGCAG AGGAGGAAAA GGTCTTAGGA GAACTGCCA ACATTTTAGA AACAGGTCTC   480
GAG                                     483

```

## (2) INFORMATION FOR SEQ ID NO:602:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:

GGGCCGTGCA GGCAGTGAAT CGGAAAGTGG AGATGATGAA TGAAAAGAAC TTGGAGAAAG	60
GACTGGGGCGT GGACAGTGTG GACAAGGATG CCATGAACGC GGCCATCCAG CAGGCCATCA	120
AGGCCCAGCC GTCCATGTCT CCCAAGAAGG CGCCCCCAGC GCCTGCAAAG GAGGCCAGGA	180
ATGTCGTGGC CGTGGGTACT GGTGGCCGTG GGACCCACGA CCGAGACCCG AGTGAGAAAC	240
CACCCCGGCT CCAAGTGGTTT GAACAGCAGG CGAAGAAGTT GGCAAAGCTA CTCGAG	296

## (2) INFORMATION FOR SEQ ID NO:603:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:603:

GAATTCGGCC TTCATGGCCT AGAACTTTT CATCTTTCCA AACAGAAATT CTATACCCAT	60
TAAACAGTAA CTCTCCCTTC ACCACTCTCC CCAACCCCGG AGACCTCTAT TCTATTTTCT	120
GTCTCTATAA ATTTGCCAT TTAGGTACC TCACATAAGT GAAATCATAT ATTTGCCCTT	180
TTGCATCTGG CTTATTTCAC TTAGCATGAT GTCTTCAAGG TTCATCCATG TGGTAGTAGC	240
AGAAATTTACT TCCTTTTAA GACTAGCATA CTCACACTGT TTTTGTGTT GTTTGTTGT	300
TTGTTGTTT TTGGGATGGA GTCTCACTCT GTTGCCCGG CTGTGGTGGC GTGGTGCCAT	360
CTCGGCTCAC TGCGGCCTCT GCCTCCCGG TTCAAGTGAT TCTCATACCT CAGCCATCCC	420
TCGG	424

## (2) INFORMATION FOR SEQ ID NO:604:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:604:

GCGATTCGAT GTCCGTGCCC ACCTGGACCA CATCCCCGAC TACACCCCCC CCTCTGCTCA	60
CCACCATCTC CCCAGAACAG GAGTCGGACG AACGGAAGTG TAACTACGAG CGCTACAGAG	120
GCCTGGTGCA GAACGACTTT GCCGGCATCT CAGAGGAGCA GTGCCTGTAC CAGATCTACA	180
TTGATGAGTT GTACGGAGGC CTCCAGAGAC CCAGCGAAGA TGAGAAGAAG AAGCTGGCAG	240
AGAAGAAGGC TTCCATCGGT TATACCTACG AGGACAGCAC GGTGGCCGAG GTAGAGAAGG	300
CACTCGAG	308

## (2) INFORMATION FOR SEQ ID NO:605:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:605:

GGATGCTACA GAAATCACAG AAGAAAGCAG AACTTCTTGA TAATGAAAAA CCAGCTGCTG	60
---	----

TGGTTGCTCC	CATAACAACG	GGCTATACGG	TGAAAATCAG	TAATTATGGA	TGGGATCAGT	120
CAGATAAGTT	TGTGAAAATC	TACATTACCT	TAAGTGGAGT	TCATCAAGTT	CCCACTGAGA	180
ATGTGCAGGT	GCATTTTACA	GAGAGGTCAT	TTGATCTTTT	GGTAAAGAAT	CTAAATGGGA	240
AGAGTTACTC	CATGATTGTG	AACAATCTCT	TGAAACCCAT	CTCTGTGGAA	GGCAGTTCAA	300
AAAAAGTCAA	GACTGATACA	GTTCTTATAT	TGTGTAGAAA	GAAAGTGGAA	AACACAAGGT	360
GGGATTACCT	GACCCAGGTT	GAAAAGGAGT	GCAAAGAAAA	AGAGAAGCCC	TCCTATGACA	420
CTGAAACAGA	TCCTAGTGAG	GGATTGATGA	ATGTTCTAAA	GAAAATTTAT	GAAGATGGAG	480
ACGATGATAT	GAAGCGAACC	CTCGAG				506

## (2) INFORMATION FOR SEQ ID NO:606:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:

GGTGAATGA	AAGATATACC	TAGAACGCCA	TCTAGAGGGA	GAAGCGAATG	TGATTCTTCC	60
CCAGAACCGA	AAGCTTTGCC	TCAGACTCCT	AGGCCGAGGA	GTCGTTCTCC	ATCATCCCCA	120
GAGCTCAACA	ACAAGTGTCT	TACCCCCCAG	AGAGAAAGAA	GCGGGTCAGA	ATCATCAGTT	180
GATCAGAAAA	CTGTGGCTCG	GACTCCCCCTG	GGGCAGAGAA	GTCGTTCCGG	ATCCTCTCAA	240
GAAGTTGATG	TGAAACCCAG	TGCATCCCCT	CAGGAAAGAA	GTGAGTCAGA	CTCTTCTCCA	300
GATTCTAAAG	CCAAGACACG	AACCCCACTT	CGGCAGAGGA	GTCGGTCTGG	ATCATCTCCA	360
GAGGTTGACA	GCAAACTCTG	ACTATCCCCT	CGGCGCAGTA	GGTCTGGTTC	CTCCCCTGAA	420
GTGAAAGATA	AGCCAAGAGC	AGCACCAGG	GCACAGAGTG	GTTCTGATTC	CTCTCCTGAA	480
CCTAAAGCTC	CAGCCCCTCG	GGCCCTTCCC	AGACAACCTG	AG		522

## (2) INFORMATION FOR SEQ ID NO:607:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:

GAATTCGGCC	TTCATGGCCT	AGGCGCACCA	AGAGCAGGGC	TGTGTGTGGG	AGGCTGCAGC	60
CAGGATTGCC	TCAGCTCCTC	CCCCTCAGGC	TGGGAGGATA	GCACAGGCTA	GGGGCTCGGG	120
GTGGAGGGTC	TCAGCTCTGC	TGCCCCCACC	CCAGTACTAG	CCTAGCTTCC	CAAGCTGTGG	180
CTTAGAGGAT	AGTTGGCTTC	CTGCCTCTCT	CCTCTAAAAT	AGCAAGTCTG	GGAAATCCTG	240
GGGTGAGTGG	AGTCACCCCA	CTCCCAGTTG	CTGGCAGAGA	CTGAGACTAA	AGCATCACTT	300
AATAAACCCC	CCAGCTCGAG					320

## (2) INFORMATION FOR SEQ ID NO:608:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:608:

GAATTCGGCC TTCATGGCCT AGTTGTGTAT TCTTTTCTCT GTATCATATG TGATAGTGGG	60
GTAGTGCCAA ACATTGTTAA CTCTGATGAA TAATGTCTCT TTTGGTTAGA TCATTCTTAC	120
CTTACTGGTA TCTCTTACTG TTTCTTACC TAGTTATGCT GTTATTGCCT ATGGCTGTGC	180
CAGCTGCCCC AAGCTAACTT GTGAGAGGGA AGGTTGCCAG ACTGAGTTCT GCTACCACTG	240
CAAGCAGATA TGGCATCCAA ATCAGACATG CGATCTACTC GAG	283

## (2) INFORMATION FOR SEQ ID NO:609:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:609:

GAATTCGGCC TTCATGGCCT ACACATGAGT GTGACCTCTG CCATGGGGAA ACACACACAG	60
AGATATCTAT ACATATATAC ATACATACAA ACATAGGCTA TCTTGGCACA CTAAATGCTA	120
AGCACTGTCT TAAGAGGTAG AGCTGGTGTG AGTGAATTA ATGTTACATT TTCCAGCTGT	180
AAACAGACAT CTGCATTTCC TAGTGAGCTG CCAGGAGCCA GATTCGGGAA CCGTAACTGA	240
TGTGCCAGGA ATGGTGCAAT GATTCCCACT TCCAGGGATC TCTCGAG	287

## (2) INFORMATION FOR SEQ ID NO:610:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:

GAATGATAGG TCCTAGGTTT AACAGGGCCC TATTGACCC CCTGCTTGTG GTGCTGCTGG	60
CTCTTCAAT TCTTGTGGTG GCTGGTCTGG TCGGGGCTCA GACCTGCCCT TCTGTGTGCT	120
CCTGCAGCAA CCAGTTCAGC AAGGTGATTT GTGTTCGGAA AAACCTGCGT GAGGTTCCGG	180
ATGGCATCTC CACCAACACA CGGCTGCTGA ACCTCCATGA GAACCAAATC CAGATCATCA	240
AAGTGAACAG CTTCAAGCAC TTGAGACACT TGGAAATCCT ACAGTTGAGT AGGAACCATA	300
TCAGAACCAT TGAAATTGGG GCTTTCAATG GTCTGGCGAA CCTCAACACT CTCGAG	356

## (2) INFORMATION FOR SEQ ID NO:611:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:

GAATTCGCCT TCATGGCCTA ACCACATGAT CCTTCGTGTT TCTTGCCTTC CATTTCCCTT	60
---	----



```

GGGTGGATGG TTGGGTAGGT GGGGTTTCCT GGT TTGGGGT TTCTCAGACA AGGGCCCTCT 120
AGGGAGGGTG CCCTGGACCC CCCACCACTC CTGGGCTGAG GAGCGTGCA CATGATGCCG 180
TTGGTGAGGT ACTGGAAGCC GTCATAGAGT TTGGTGGTGA TAGACCGCAT ACTGCCATCC 240
ACCATCTGCT CCACCAGCAG CTGCAGCTGC TCCTCAGTCA TGCTCATGTG GAACCTCTCT 300
TTGAGGTTNC GAATGGTGCT GGAGCCATGG AAGCAAGGAA GCTGAGAACC TTGTCCATGT 360
GTTTCCGAGC GGCAATCAGC CCTTGCAGCA TCA 393

```

## (2) INFORMATION FOR SEQ ID NO:612:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 645 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:

```

GAATTCGGCC TTCATGGCCT AGGCGGGTTA AAGTCACATT TTTAAAAAGG CTAAACTCTA 60
AATTGCTGTA TTTGCTCTCT CTGGAGATTA ACAAAGTGCT TGGTTTGCGAG ATTGCTGGT 120
ACGGTGATCT CAATGATATG ACCGAGGGTG GGAGGGATGT GAGGAGGGAA ATCGGCAAAA 180
CCCTGGCCAG CCAGCCAGCC AAGGTGACAC ACAGCCAGAG GGGGCTCCCC TCTCCTCCTG 240
CCGTCCGGCC ACGGCTCACC ACGCTGTCCA CTGGGAACGC GGCCCCGCGG CCCGCAGAGT 300
CAGGCGTGAG CTTGCCCTT TTCTGAAAGG GCCTCCGCCT GGGCAGGCGC CGGGGGGCAG 360
TCCTCGGGTC CCATGGCTTA GGAGCACAGC ACTGACGGCT GCAGTGGCTC GAAAGGCTGA 420
AATTCCACAT TGCTCTCTAG CGATCCCGCA CTGCTGCGAC GCCCTCGCTT CCCGGCTTCC 480
GAGAGTCCC GCAGGGAGCT GCTGAGGGCG CTGCGCTTGA GGCCCTCACC GCTGGCATAG 540
CTGTCGTCCA GGCAGGCCCC GCTCAGTGT TCCGTTGCCC GACTCCTTTT TGAGGCTAGA 600
GCACTGGGAC ATGCTGGGCC GCACGACGCC TTTCTGCTTC TCGAG 645

```

## (2) INFORMATION FOR SEQ ID NO:613:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:

```

GCGATTGAAT TCTAGACCTG CCTCGCACCA CCCCAAATCC CACATCCTGC ACCCCTGCCT 60
CAGGCTTCCT GCCCTCAACC CCAATATTCT GAGCCTTCTC TTTTTTTTTG TTGTTTTTTT 120
GAGACAGAGT CTTGCTCTGT CTGTGCGACA GGCTGGAGAG CAGTGGCGCG ATCTCAACTC 180
ACTGCAACCT TCACCTCCCA GGTTCAGCA ATTCTCCTGT CTCAAGTGCC TAGATACCTT 240
GGTAATGATT CCATTGGCCC CACCATGCCC TGTCCTGCCT TCCTGGCTGT GCCCAAGCTT 300
GGTCCCTGCC TGCCTGCCTC ACTCTCTGGG TCTCGAG 337

```

## (2) INFORMATION FOR SEQ ID NO:614:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:

```

GAATTCGGCC TTCATGGCCT AGGTTTTAGA ATTTTATATG AAGTATCTTA TTTGATTTTC      60
ATAATAACCA TAGAAGATAG ATACTATTAT TATCCTTGGA TTATAGATGA AATTGAAGAT      120
TGCTTCGCAG GTAGAGTTAA GATCCAGAAT GGTGACAAGA AGTATAATGT CTGCTTTTAT      180
GCCATAATAT ATCAGACTAT TCTGACTCAT TTAGATTACT TCAGGGCTAT CACTGAAGCT      240
TACAGTATTA TCACTACTGT GATACCCCTG CTCACACAAT TTGGTAAGTG TTTTGTATC      300
TTTTAGAACT TATACATTAG GCAGCAGCTA TCTGTTTGGT CAGCTGAAAG ACGGCCACAG      360
GATTTGCTTC TGGGTGGCCA TTAGCACCTT TCACCCATGC ACCAGAGAGA TACTTCCAGC      420
ACGAACTCGA G                                     431

```

## (2) INFORMATION FOR SEQ ID NO:615:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:

```

GAATTCGGCC TTCATGGCCT ACCAAAATTG TGCATACCCT TGGGATGAAA ATCATTGTAA      60
AGAAAAGAAA AAAGCAGGAN TATTTGAACA AATCACTAAA ACTCATGGAA CAATTTTGG      120
CATTACTTCA GGGATTGTCT TGGTCCTTCT CATTATTCT ATTTTAGTAC AAGTGAAACA      180
GCCTCGAAAA AAGGTCATGG CTTGCAAAAC CGCTTTTAAT AAAACCGGGT TCCAAGAAGT      240
GTTTGATCCT CCTCATTATG AACTGTTTTT ACTAAGGGAC AAAGAGATT CTGCAGACCT      300
GGCAGACTTG TCGGAAGAAT TGGACAATA CCAGAAGATG CGGCGCTCCT CCACCGCCTC      360
CCGCTGCATC CACGACCACC ACTGTGGGTC GCAGGCCTCC AGCGTCAAAC AAAGCAGGAC      420
CAACCTCAGT TCCATGGAAC TTCCTTTCCG AAATGACTTT GCACAACCAC AGCCAATGCT      480
CGAG                                     484

```

## (2) INFORMATION FOR SEQ ID NO:616:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:616:

```

GAATTCGGCC TTCATGGCCT AGCGTTCCTG GTTCCGTCCT TGTACATAAT ATTGTACAGC      60
ATTCAACCAC TTTTGTCTGAT CAGCAAAGTA GTCTCCAATG GCATTGTTGG CTTGTTCCAG      120
GAGACTGTCA TCTGCATCAC CAGATCCAGT TTTCAGGAGC TGGAGTACTC TAAACCAATC      180
CCCCAATTTC AGCCGGAGGC CAATAGCAAG ATCCCTTCTG TCCATCTCGA G               231

```

## (2) INFORMATION FOR SEQ ID NO:617:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 627 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:617:

```

GAATTCGGCC TTCATGGCCT ANAATGCTTC ATGAAGTNGC NGACAGGACT GACACAGCTN      60
AGCTTTTCTG ACTGATTTCG GGCCATGCAG TCTACCAAAG GGCTAGCTGT TGAGACAATG      120
AGGATCAGGG ACATTTGCCC TCGTTCTGAA TGTCCCCAGC CACAGTACNT ACATNGTTCT      180
TACATGTACC TTCCCCCTCG GTGACATTTT ATATTTTCCA AGNTGGCCAC ANCNGTTCCT      240
TTCCCTTTCT NNTNGNGNNG NACACTCACA CCGTCTCTG NGAGGTGAGG CCACATATTC      300
TCTTTTCTGG AATTGGGGTG GGCCTGTGAC AATGGCAGGA CAATGCTGAG TGGCTATGTC      360
ATAAAGGCAA TACCCCTTCC ATCCAATTCT CTTGGGATGC TCATGTTTAG AATCCAGCCA      420
CCATGTTGTG AGGAAGCCCA CGTCACCTAT GAAGACCTAC ACAGAAAAGA CTCAAGGCCC      480
CAGGCACCTG AGCTGAAGGA TGAAAAAGAG TTAGTCAGCA GGGGAAATTG GGGAAAGGGT      540
ATCTGGTAGA AAGAAGGAAC AGCTTGTGCA GAGGTNCAGA GGCAAGAGAG AATTTGGCAT      600
ATTGCGGAAG CTGCAAAAGA TCTCGAG                                     627

```

## (2) INFORMATION FOR SEQ ID NO:618:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:618:

```

GAATTCGGCC TTCATGGCCT ACGACTTCAA AAATATGGGA ACACAGTTAG TTATTTTAC      60
ACACTTCTTT TTGTTTTTGT GTGTGTGTGC TGTCGCTTGT CGACAACAGC TTTTGTGTTT      120
CCTCAATGAG                                     130

```

## (2) INFORMATION FOR SEQ ID NO:619:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:619:

```

GAATTCGGCC TTCATGGCCT ACTGGGGGAG GGGGAAGGATG TGGTTTGNAG AGNGGAAGCA      60
GAGTTTGGAA ACGCATGAGA GCAGAGCTTC GTGTGTTCCC ACCCTCANTG AGGANGTGTG      120
AGTGGGTGAG CATGTGAGAG TTGGGTGTTT CTACCCTCAG TGAGGAGGTG TGAGTGGGGG      180
TGCAATATAGA GGCAGTGCCT GCTGTGGGGT CACAACCTGGT GCATGCCAGC GCCAAAGGGA      240
CCTGTCTTTA GGGGTCAATT CAGCCAGCTC CTCCCATCAC ACATGACAGC TCCAAGCCTA      300
GAAGGGGCTC AGTGACAGGG CCAGGACAAG CCCTCAGGAC TGTGGCCTCC TGGCCCTTGG      360
TTCCCTGCCC CCACAACATG GTCTCCACAT GGCTGGCTGG CTGGCTGTCC CTGTGTGTGT      420
GTGACACACG GTGTGAGTGC AGGGCTGTGC CCGGGGTGGG AGGGTGTCTA TGTGGCACTG      480
ACTATCGAGC TCGAG                                     495

```

## (2) INFORMATION FOR SEQ ID NO:620:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear